

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 23, 2005, 19:27:11 ; Search time 27 Seconds  
(without alignments)  
1607.176 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAFKQLDTLGLPGLLSIY.....EDMDRLKADKWKYQYVG 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2314	99.1	451	2 T43733	trichothecene 3-O-
2	962.5	41.2	474	2 S50957	probable membrane
3	151.5	6.5	459	2 T45576	anthranilate N-hyd
4	150.5	6.4	430	2 T46216	hypothetical prote
5	149.5	6.4	450	2 T45573	anthranilate N-hyd
6	149	6.4	648	2 T45575	hypothetical prote
7	146	6.3	443	2 T45574	anthranilate N-hyd
8	143	6.1	475	2 T45961	anthranilate N-ben
9	141.5	6.1	436	2 D86378	protein F21J9.8 [i
10	132	5.7	439	2 T52321	taxadienol acetyl
11	131.5	5.6	433	2 H84826	hypothetical prote
12	130.5	5.6	451	2 T00527	hypothetical prote
13	126.5	5.4	435	2 E71418	hypothetical prote
14	124.5	5.3	450	2 T48479	hypothetical prote
15	124	5.3	445	2 T10717	anthranilate N-ben
16	121.5	5.2	482	2 G84823	probable anthocyan
17	118.5	5.1	480	2 H86411	protein Flk23.12 [
18	118	5.1	440	2 T02368	hypothetical prote
19	117	5.0	442	2 T10718	anthranilate N-ben
20	115.5	4.9	446	2 T10711	anthranilate N-ben
21	115	4.9	838	2 T13102	probable minor tai
22	113.5	4.9	3436	2 S55659	tegument protein 6
23	113	4.8	440	2 T52320	10-deacetyl bacati
24	111.5	4.8	575	2 D64998	hypothetical prote
25	109.5	4.7	451	2 T01140	hypothetical prote
26	109	4.7	445	2 T10719	anthranilate N-ben
27	105.5	4.5	446	2 D71418	hypothetical prote
28	105	4.5	1825	2 C88400	protein H19M22.1 [
29	105	4.5	1825	2 T32828	hypothetical prote

30	104.5	4.5	464	2 T45612	N-hydroxycinnamoyl
31	104.5	4.5	1337	1 I38670	protein-tyrosine-p
32	104	4.5	1896	2 T08851	Down syndrome cell
33	103.5	4.4	458	2 T06313	hypothetical prote
34	102.5	4.4	762	2 E98121	hypothetical prote
35	102.5	4.4	810	2 D95256	ATP-dependent Clp
36	102	4.4	753	2 A86756	prophage pi2 prote
37	101.5	4.3	465	2 D86166	protein F21B7.12 [
38	101.5	4.3	904	2 S51299	hypothetical prote
39	101.5	4.3	7576	2 T17428	FK506 polyketide s
40	101	4.3	363	2 T08542	mitogen-activated
41	101	4.3	363	2 T51735	mitogen-activated
42	101	4.3	761	2 A53414	A-kinase anchor pr
43	100.5	4.3	963	2 T09911	probable serine/th
44	100.5	4.3	1868	2 S48938	hypothetical prote
45	100	4.3	461	2 H84644	hypothetical prote

ALIGNMENTS

RESULT 1

T43733  
trichothecene 3-O-acetyltransferase [imported] - Gibberella zeae (subsp. graminearum)  
C:Species: Gibberella zeae  
A:Variety: subsp. graminearum  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T43733  
R:Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.; Yamaguchi, I.  
PEBS Lett. 435, 163-168, 1998  
A:Title: The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the re  
A:Reference number: Z22654; MUID:98433864; PMID:9762900  
A:Accession: T43733  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-451 <KIM>  
A:Cross-references: UNIPROT:O42692; EMBL:AB011417; NID:g3724288; PIDN:BA333768.1; PID:g3  
A:Experimental source: strain F15  
C:Genetics:  
A:Gene: Tril101

Query Match 99.1%; Score 2314; DB 2; Length 451;  
Best Local Similarity 99.1%; Pred. No. 6e-168;  
Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	MAFKIQLDTLGLPGLLSIYTOISLLYPVSDSOYPTIVSTPEQGLKRFESEAVPWAGQV	60
DB	1	MAFKIQLDTLGLPGLLSIYTOISLLYPVSDSOYPTIVSTPEQGLKRFESEAVPWAGQV	60
QY	61	KAEGISSEGNLTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK	120
DB	61	KAEGISSEGNLTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK	120
QY	121	TLPIGSGTGPDGPKPVILLQLNFIKGGLILTVNGQHGAMVQDQDAVIRLLSKACRNDPF	180
DB	121	TLPIGSGTGPDGPKPVILLQLNFIKGGLILTVNGQHGAMVQDQDAVIRLLSKACRNDPF	180
QY	181	TEEMTAMNLDKRTIIVPLENTTIGPEVDHVIKADVAGDAVLTVPVSASWAFETSPKA	240
DB	181	TEEMTAMNLDKRTIIVPLENTTIGPEVDHVIKADVAGDAVLTVPVSASWAFETSPKA	240
QY	241	MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVLRIIDGSAFTEFCRAVDARPMG	300
DB	241	MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVLRIIDGSAFTEFCRAVDARPMG	300
QY	301	VSNVYFGLLQNMTHYNTTIGETANESLGATASRLRSELDPSASNRQTRGLATYLVHNPDK	360
DB	301	VSNVYFGLLQNMTHYNTTIGETANESLGATASRLRSELDPSASNRQTRGLATYLVHNPDK	360
QY	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVSLSMYFMPKKPD	420
DB	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVSLSMYFMPKKPD	420

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QY 421 GEFCAALSRLDEMDRLKADKEWTKYAQYVG 451
Db 421 GEFCAALSRLDEMDRLKADKEWTKYAQYVG 451

RESULT 2
S50957
probable membrane protein YLL063c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L0549
C:Species: Saccharomyces cerevisiae
C>Date: 10-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S50957; S64815
R:Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cerevisiae
A:Reference number: S50950
A:Accession: S50957
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: UNIPROT:Q12226; EMBL:Z47973; NID:G642313; PID:G642321
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64815
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: UNIPROT:Q12226; EMBL:Z47973; NID:G642313; PID:G642321
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64815
A:Molecule type: DNA
A:Residues: 1-474 <WED>
A:Cross-references: EMBL:Z73168; NID:G1360275; PID:G1360276; MIPS:YLL063c
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGP:AYT1
A:Cross-references: SGD:S0003986
A:Map position: 12L
A:Keywords: transmembrane protein
F:153-169/Domain: transmembrane #status predicted <TMM>

Query Match 41.2%; Score 962.5; DB 2; Length 474;
Best Local Similarity 44.4%; Pred. No. 3e-65;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDLTGLQLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGQVKAEG 65
Db 22 QLDLTGLQLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGQVKAEG 65

QY 66 SEGNTGTSTFVPPEDVPRVVKDLRDDPSAPTIETGMRKAGYPMAMFENIIAPRKL-PI 124
Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSEKADFPIYMLDEKTFAPCMTINPP 140

QY 125 GPOTG-PDDPKPVILLQINFKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPTEE 183
Db 141 GNTIGMAAKSGPVFAQANFISGLGLVITVNGQHGAMDMVGQDAVIRLLSKACRNDPTEE 200

QY 184 EMTAMNDRKTIYVPLENTYIGPEVD--HQIVKA--DVAGGDVAVLTPVS-ASWAPFTFSP 238
Db 201 ELLIGNIDKSKSIPLFDE-TWEPDTLVVHIVTSNTSGEEKEQSCSSNTHWAYVEFSA 259

QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFKSASRVRLERIDGSAFCEAVDARPA 298
Db 260 ISLQNLRIILAMQCTSGTFVSTDDIVTAFIWKSVSRKRLSKLPETKSNLGRAVDVRKR 319

QY 299 MGVSNNYPGLLQNMVTHNSTIGIANESLGATASRLSELDPDPA--SMRQRTGLATYLN 356
Db 320 LGLPETYPGLLVNMTNTGSLKSLDKSLGSLASQIRKRLDPKVFPLAVNTCALATLSR 379

QY 357 NPKDSNVSLTADAPDSTVMSLWAKVGLWDYDFGLGKPFVTRPIPEPVESLYMFMP 416
Db 380 CPDKTKVSIPOPTIDTISLVINSSWAKVSLVDVDFNLGLGKPKSVRRPRFISLESLLYFMP 439

QY 417 KKPDPGFCALSRURDEMDRLKADKEWTKYAQYVG 451
Db 440 RSSRGEMWVALCLRDQWECLNADKEWTKYATHIG 474

RESULT 3
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T45576
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana
N:Alternate names: protein FllC1.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45576
R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Maye
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <BAR>
A:Cross-references: UNIPROT:Q9SND7; EMBL:AL132976
A:Experimental source: cultivar Columbia; BAC clone FllC1
C:Genetics:
A:Map position: 3
A:Introns: 445/3
A:Note: FllC1.140

Query Match 6.5%; Score 151.5; DB 2; Length 459;
Best Local Similarity 22.5%; Pred. No. 0.0011;
Matches 95; Conservative 64; Mismatches 189; Indels 75; Gaps 17;

QY 4 KIQLDTLGLQLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGQVKA 61
Db 24 KIHL-TPSDLSLLYLNYPQRLFFP---KPYPTFRFISRLKSSLSLSTLEIYFPLAGRLV 78

QY 62 AEGISEGNTGTSTFVPPEDVPRV-VVKDLRDDPSAPTIETGMRKAGYPMAMFENIIAPRK 120
Db 79 KVNNEHNT-VSFYDCDDGRCVKFHAIESVSV-----SDILQPHG 120

QY 121 TLP-----IGPGTGPDD----PKPVILLQINFKGLLITVNGQHGAMDMVGQDAVIRLL 171
Db 121 SVPDFRFLFPVNGVRSIDGLSEPLLAQVTEIKGIVISFGVNLVADGSSWNNFHVW 180

QY 172 SKACRNDPTEEMTAM-----NLDKRTIYPLENTYIGPEVDHQIVKADVAGGDAVLT 225
Db 181 SKLCLNGQWEIHQPLVLRGWFNDNDFPIHIP-----ASEIETEARNR 224

QY 226 PVSASWAFPTFSKAMSELKDAATKTLDASTKFSVSTDDALSAPFKSASRVRLERIDGSA 285
Db 225 EVSTKERVHFHFKELSLDKAKANDEIGSSDIKISLQAVLAHLWRSI--VRHSGLNQEE 282

QY 286 PTEFCRAVDARPAWG--VSNNYPGLLQNMVTHNSTIGIANESLGATASRLSELDPASM 343
Db 283 ESRGCGVAADFQRLNPPLDKDCFGNVANGLTATVGDLLDRGLGWAALQINK-----TV 337

QY 344 RQRT-RGLATYLN--NPKDSNVSLTAD-ADPSTVMSLWAKVGLWDYDFGLGKPKPE 398
Db 338 RLHTNENFTFSNVWRNGKIPRIDVSRMGDFGFWNSPWFQV----YDNDFGLGKPM 393

QY 399 TVR 401
Db 394 AVR 396

RESULT 4
T46216
hypothetical protein T8P19.230 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46216
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23008
A:Accession: T46216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-430 <CHO>
A:Cross-references: UNIPROT:Q9SMM7; EMBL:AL133315
A:Experimental source: cultivar Columbia; BAC clone T8P19
C:Genetics:
```

A;Map position: 3  
A;Introns: 144/3  
A;Note: T8P19.230  
C;Superfamily: Arabidopsis CER2 protein

Query Match      6.4%; Score 150.5; DB 2; Length 430;  
Best Local Similarity    20.3%; Pred. No. 0.0012;  
Matches         95; Conservative    61; Mismatches    163; Indels    149; Gaps    19;

Qy                  25 LLYPVSSSQYPTTVSTFEQGL-----KRFSEAVPW--V 56  
Db                  16 LIIPVSETPNGHYVLSNLDQNIAIVKTLLYYKSESRTNOESNVVKSLSEVLVHVPV 75  
  
Qy                  57 AGQ--VKAEG-ISGNTGTSPVFEDVRVVKKDLRDDPSAPTIEGRKAGYPMAFMDE 113  
Db                  76 AGRLTISPGEKIAVNCTGCVWV-VAAEANGCIDTIKEAISERNMETLEKLIV----- 127  
  
Qy                  114 NIAPRXTLPICPGTGPDDPKPVILLQLNFITKGLILVTNGQHGMVGDVIRLLSK 173  
Db                  128 DVGARNILEI-----PPVVVQTNQFGGVFLGLGNSHNMFDGV---AAAEFINS 175  
  
Qy                  174 ACRN-----DPFTEEMTNMLDKRTIIPYLENTIGPEVDHQIVKADVAGDAVLT 225  
Db                  176 WCENAKGLPLSVPFPIORTILRSNPPIKEFHNEPDEL-----EDISTGKIYD 225  
  
Qy                  226 PVSASWAFFTFSPKAMSELKDAAATKTLIDASTKFYSTDDLASFATWSASKRVRLERIDGSA 285  
Db                  226 BEKLIYSFLFEPEKLEKIMATE--ENNKNKYSTFTQALTGFLLKSR----- 271  
  
Qy                  286 PTEFCRAVDARP-----AMGVSNYPOLLON-----MYHNSTIGEIANE 325  
Db                  272 ----CEALREFKPDOVKLLFAADGRSFRIFPRLPQGCGNGIVLTGLVTSSGELVGNPLSH 327  
  
Qy                  326 SLG-----ATASRLRSELDPASMQRTRGLATYLHHNNPDKSNSVLTADADFSTSVML 377  
Db                  328 SVGLVKKLVELVTDGFWRSAMD-----YEVNRTFSMNAI-----LLI 366  
  
Qy                  378 SSWAKVGLWDYDFGLGLGKPEPTRRRPIPE-----PVESLMYFMFKPKD 420  
Db                  367 TSWSKLTHLKLDLCWG-----EPVFGSGVGLPGREVILFLPSGGD 406

RESULT 5  
T45573  
N;Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C;Accession: T45573  
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May,  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: Z23007  
A;Accession: T45573  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-450 <BAR>  
A;Cross-references: UNIPROT.Q9SNEO; EMBL.ALJ132976  
A;Experimental source: cultivar Columbia; BAC clone Fllc1  
C;Genetics:  
A;Map position: 3  
A;Note: Fllc1.110

Query Match      6.4%; Score 149.5; DB 2; Length 450;  
Best Local Similarity    21.2%; Pred. No. 0.0016;  
Matches         97; Conservative    71; Mismatches    207; Indels    83; Gaps    19;

Qy                  20 YQISLLYLVSDSSQYPTTVSTFEQGLKRFSEA-VPWVAGOVKAEGISE-----GN 69  
Db                  41 YPQGLLFSEKPD-SDFHLIIISRKDSLSLALEYFPFPAAGRVLTKTENLEDTTVSFFIDCDG 99  
  
Qy                  70 TGTSFIVPFEDVRVVVKD-LRPDPSAPTIEGRKAGYPMAFMFENITAPRKTLPIQGGT 128  
Db                  100 SGARFL--HTEAHSVSDILOPPGSVP----DFUKFYFP----- 133

QY 410 SLMYFMPKPDGDFCAALSLRDEMDRLKAD 440  
Db 417 KLRKFW--RPRTEL-RSIVQREKDGKMESE 444

RESULT 7  
T45574  
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein - Arabidopsis thaliana  
N/Alternate names: protein F11C1.120  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C/Accession: T45574  
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, December 1999  
A/Reference number: 223007  
A/Accession: T45574  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-443 <BAR>  
A/Cross-references: UNIPROT:Q9SND9; EMBL:AL132976  
A/Experimental source: cultivar Columbia; BAC clone F11C1  
C/Genetics:  
A/Map position: 3  
A/Note: F11C1.120

Query Match 6.3%; Score 146; DB 2; Length 443;  
Best Local Similarity 22.6%; Pred. No. 0.0028;  
Matches 103; Conservative 62; Mismatches 204; Indels 86; Gaps 19;

QY 20 YTOISLLYPVSDSQPTTVSTPEQGLKRFSEAVPWVAGQV-KAEG-----ISEGN 69  
Db 39 YTORGLLPKPDPEH--FISRLTSLSSALDIYFPFAGRLNKVENHEDETVSFYINCDS 96  
QY 70 TGTSTFIVPDEVRVVVKD-LRDDPSAPTIEGMRKAGYPMAMPDENIIAPRKLTPGPGT 128  
Db 97 SGAKFTHAVSD--SVSVSDLLRDPDGV--DPFRIFYPM-----NGV 134  
QY 129 GPDD--PKPVILLQLQFIKGLLLTVNGOHGAMDMVQDAVI-----RLLSKACRN----- 177  
Db 135 KSIDGSEPLALQVTEMDGDFVIGFYNH-----WVADGASIWNFRTWSKICSNQOREN 190  
QY 178 -DPFTEEMTAMNLDRTKIIPVLENYTIQPEVDHQIVKADVAGGAVLTPVVSASWAFPT 236  
Db 191 LQPLALKGLFVDGMDFFIHIPVSDTETSPSRE-----LSPTFKE-RVFHF 235  
QY 237 SPKAMSELKDAATKTLDASTKTVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDAR 296  
Db 236 TKRNIIDLKAKVNGEIGLRDHKVSLSLQAVSAHMRISI--IRHSGLNQBEKTRCFVAVDLR 293  
QY 297 PAMGVSNVYFGLLQNNYTH-----NSTIGETANESIGATASRLRSELDPASMRQTRG 349  
Db 294 QRLN-----PPLDKECFHVYNSVTVTIGELHDOGGLWAFGLQINMLRSLTNEDYRIY 348  
QY 350 LATYLHN-NPDKSNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGLGKPTVRRPIFEVP 408  
Db 349 AENWVNMKIQKSLGSKMTRD--SVIVSSSPRFEVDNDF--GWGKPIAVRAGFSNFI 403  
QY 409 ESLMYFMPKPDGEFCAALSLRDEMDRLKADKEW 443  
Db 404 SGKLVFRFGTIEGCIDVHAFLLPDLVLVGLADVEF 438

RESULT 8  
T45961  
anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana  
N/Alternate names: protein F7J8.190  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C/Accession: T45961  
R/Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lem  
submitted to the Protein Sequence Database, January 2000  
A/Reference number: 223018

A/Accession: T45961  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-475 <BEV>  
A/Cross-references: UNIPROT:Q9LFB5; EMBL:AL137189  
A/Experimental source: cultivar Columbia; BAC clone F7J8  
C/Genetics:  
A/Map position: 5  
A/Note: F7J8.190

Query Match 6.1%; Score 143; DB 2; Length 475;  
Best Local Similarity 19.7%; Pred. No. 0.0053;  
Matches 103; Conservative 71; Mismatches 190; Indels 158; Gaps 20;

QY 9 TLGQLPGLLSIVTQIS-LLYPVSDSQPTTVSTPEQGLKRFSEAVPWVAGQVKAEB---- 63  
Db 28 SVSDLPMLSCHVIQKGVLLTSPPPSFDDLVSSLRSLSSLTSLFPALAGRFSTTPAGH 87  
QY 64 -GISEGNTGTSFI-----VPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPM 109  
Db 88 ISIVCNDAGVDFAASAKHVKLSLDVLLPGEDVP-----L 121  
QY 110 MFDENIIAPRKLTPGPGTDPDPKPVILLQLNFIKGLLTVNGOHGAMDMVG-----QD 165  
Db 122 LFRFPFVFERLVSYNG-----HHRKLAQVQTELDHGVFIGCTVNHSTVDGTSFWMHFFN 175  
QY 166 AVIRLLSKACRNDPTEEBMTAMNLDRTKIIPVLENYTIQPEVDHQIVKADVAGGDAVLT 225  
Db 176 TPADTVSGACK-----IKHLPDFSRHTVDFSPVLPVPFGGPRVTFF 216  
QY 226 PVSASW--AFFTFSPKAMSELKDA-----TKTLDA----- 254  
Db 217 DADQPLRERIFHFSREATIKLKORTNNRVNGIETAVNDGRKCNKEINGKITTVLDSFLNN 276  
QY 255 -----STKFEVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDAR-----PAM----- 299  
Db 277 KKSVDRTAEISSQSLSAQLMRSVTRAR--NLDPSKTTTFRMAVNCRRHLRPMDDPYFG 334  
QY 300 GVSNNYPGLLQNNYTHNSTIGETANESIGATASRLRSEL---DPASMRQTRGLATYLHN 356  
Db 335 NAIQSIPTL-----ASAGLLSKDLSEAEQLHRNVVAHDDATVR---RGIAAWESD 383  
QY 357 -----NPDKSNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGLGKPTVRRPIFEVE 409  
Db 384 PRLFLPLGNPD-----GASITWGSSPRFPMYDNDF--GWGKPLAVRSGGANKFD 429  
QY 410 SLMYFMP-KKPDGEFCAALSLRDEMDRLKADKEWTKYAYV 450  
Db 430 GKISAPFGREGNSVDLEVLAPETMTGIENDAEFMQYVSEV 471

RESULT 9  
D86378  
protein F21J9.8 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: D86378  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.P.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: D86378  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-436 <STO>  
A/Cross-references: UNIPROT:Q9FYM1; GB:AE005172; NID:g9743331; PIDN:AAF97955.1; GSPDB:GN



Db 228 -----TYFIIDFTINIKOS-----VMECKEFCSCFEVASATW--IARTAFQIPSE 276  
 Qy 286 PTEFCRAVDARPAMGVSNYPLGLQNMTYHNS--TIGEIANESLGATASRLRS-----ELD 339  
 Db 277 YVKILFGMDMR-----NSFNPLPSGYGNSIGTACAVDNVQDULLSGSLLRAIMIIKKS 330  
 Qy 340 PASMRQRTGLATYLNHPDKNSVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEP 399  
 Db 331 KVSINDNFKRAVV---KPSELDVMNMHSE---NVVAFADWSRLGDFEYDFGWNASVVS 383  
 Qy 400 VRRPIEPVESLM--YFM-----PKKPDG 421  
 Db 384 ---PVQOQSALAMQNYFLFXPKSKNKPDC 409  
  
 RESULT 11  
 H84826  
 hypothetical protein At2g40230 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: H84826  
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; G.  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197  
 A/Accession: H84826  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-433 <STO>  
 A/Cross-references: UNIPROT:Q9XEF2; GB:AE002093; NID:g6598942; PIDN:AAF18737.1; GSPDB:GN(GN  
 C/Genetics:  
 A/Gene: At2g40230  
 A/Map position: 2  
  
 Query Match 5.6%; Score 131.5; DB 2; Length 433;  
 Best Local Similarity 22.7%; Pred. No. 0.035;  
 Matches 67; Conservative 54; Mismatches 97; Indels 77; Gaps 17;  
  
 Qy 135 PVILLQLNFIK-GGLITVNGQHGMVMDVGDAVIRLLSKACRNDPFTTEETAMNL-DR 192  
 Db 137 PPLVVQVTLWRDGAALAVGNHCVSDIGSAEFTLFAELSK-DLSQTELRKRHLNDR 195  
 Qy 193 KTIVPY-LENYTIGPEVDHQIVKADVAG-----GDVLTTPVSASWAFFTFSPKAMSELKD 246  
 Db 196 QLLMPSPIRDSLSHPEFNR---VPDLGCFVNRFAERLVPTSV-----VFERQKLNELKK 247  
 Qy 247 AATKTLDASTKFTVTDALSFIWKSAR-----VRL-----BRIGCSAPTEF- 289  
 Db 248 LASRLGEFNSKHTSF-EVLSAHVWRVSWARSLNLPNSQVLLKLLFSVNIIRDVXPSLPSGFY 306  
 Qy 290 -----CRAVDARPMGVSNYFCLQNMTYHNSSTIGEIANESLGATASRLSELDPAS 342  
 Db 307 GNAFVVGCAQTTVKDLTEKGLSYATMLVKQ-----AKERVG--DEYVRSVVEAVS 354  
 Qy 343 MRQRTGLATYLNHPDKNSVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEP 397  
 Db 355 -KERA-----SPDSVGV-----LILSQWSRLGLEKLDLF--GLGKP 386  
  
 RESULT 12  
 T00527  
 hypothetical protein At2g19070 [imported] - Arabidopsis thaliana  
 N/Alternate names: hypothetical protein T20K24.8  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
 C/Accession: T00527; B84572  
 R/Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, E.  
 submitted to the EMBL Data Library, July 1997  
 A/Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.  
 A/Reference number: Z14167  
 A/Accession: T00527

A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-451 <R0>  
A;Cross-references: UNIPROT:O64470; EMBL:AC002392; NID:g3176701; PID:g3176709  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.  
eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: B84572  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-451 <R0>  
A;Cross-references: GB:AE002093; NID:g3176709; PIDN:AA12025.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g19070; T20K24.8  
A;Map position: 2  
A;Introns: 322/1

Query Match 5.6%; Score 130.5; DB 2; Length 451;  
Best Local Similarity 21.1%; Pred. NO. 0.044;  
Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;

QY 8 DTLGQLPGLLSIYTOISLLYPVSDSQYPTIVSTFPGQLKRFSEAVPWVAGOVK----- 61  
Db 29 DQVGTTHIPTLY-----FYDKSESFGQNVVBLKTSLSRVLVHFPVPMAGRLRWLPRGR 83  
QY 62 -----AEGI-----SEGNTGTFIVPPEDVPRVVVKDLRDPSPAPTIEGMRKAGYPMA 109  
Db 84 FELCNAGVEFTEASEGK-----LSDFKDFSPTEFENL----- 119  
QY 110 MPDENIAPKTLPIGPGTDPDPKPVILLQLNFI--KGLILTVNGHGMVQDAMVGDV 168  
Db 120 MPQVYKNPIETIPL-----FLAQVTKFKGGISLSVNVSHAIVD--GQSA-L 164  
QY 169 RLSS-----KACRNDPFTTEEMTANLDRKTI---VPYLENTYIGPEVDHQ----- 211  
Db 165 HLISEWGLRARGEPL---TVFFLDKILWAGEP-LPPVSPPKDFKDFDQPPFLIGE 219  
QY 212 --IVKADVAGDVLTPVVSASWAFSTPKAMSELKDA--TKTLASIKFVSTDDALSA 267  
Db 220 TDNVVEERKKTIVVMLPLSTS-----OLQKRSKANGSKHSDPAKGF-TRYETVTG 269  
QY 268 FINKSASRVLERIDGSAPEFCRAVDAPAM--GVSNYPGLLQNMVTHNSTIGSIANE 325  
Db 270 HVWRCACAKGH--SPQPTALGICIDTRSEMPPILPRGYFGNATLDVVAASTSGELISN 327  
QY 326 SLGATASRLSELDPSMRQRTGLATYLHNNPD-KSNVSLTA-----DADPSTSV 376  
Db 328 ELGFAASLSKAIKNVTNEYVMIGI-BYLNQKDLKKFQDLHALGSTGEPFYGNPNLGV 386  
QY 377 LSSWAKVGLWDYDFGLGKPEVTRRPIFEPVESLMYFMP-KKPDGEFCAALSIRDEMD 435  
Db 387 --SMLTLPMTYGLDFGWG---KEFTGTGTHDFDGSILILPDQNEGDSVILATCLOVHME 441  
QY 436 RLK 438  
Db 442 AFK 444

RESULT 13  
E71418  
hypothetical protein - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
A;Variety: Columbia  
C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
C;Accession: E71418  
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel  
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,  
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc  
C.; Chalwatzis, N.  
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali  
A;Reference number: A71400; MUID:98121113; PMID:9461215  
A;Accession: E71418  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-435 <BEV>  
A;Cross-references: UNIPROT:O23393; GB:Z97338; NID:g2244870; PID:e336926; PID:g2244897  
C;Genetics:  
A;Map position: 4COP9-4G3845

Query Match 5.4%; Score 126.5; DB 2; Length 435;  
Best Local Similarity 20.2%; Pred. NO. 0.084;  
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

QY 4 KIOLDTIG-QLPGLLSIYTOISLLYP-VSDSQYPTIVSTFTEOGLK-----RFEAVPWV 56  
Db 23 RLQSLDLXCFG---IYVSTIFFYDLTISE-----VFSNKLKLSLSETLRFPY-L 72  
QY 57 AGOVKAEGISEGNTGTSFIVPPEDVPRVVVKDLRDPSPAPTIEGMRKAGYPMAMPDENII 116  
Db 73 AGRIEGLSISCNDEGAVTEARTD---LLLPDLFLNLNTDSLGSF----- 114  
QY 117 APRKTLPI-IGPGTGDDPKPVILLQLNFI--KGLILTVNGHGMVQDAMVGDVIRLLSK 173  
Db 115 -----LPTLAAGESP-AAWPLLSVKVTFGSGGVAVSVSHKTCIDIASLVTFVK--- 164  
QY 174 ACERNDPFTEEMTANLDRKTI-VPYLENTYIGPEVDHQIVKADVAGDVLTPVVSASWAF 233  
Db 165 -----DWAT---TTAKGKSNSTI-EPAETIYPPPSHMYEQFPSTDSNIT---SKYVL 213  
QY 234 --FTFSPKAMSELK-DAATKTLDASTKFTVSTDDALSAPFWKSA----- 273  
Db 214 KRFVPEPSKIAELKHAASESVFVPTRV---EATMSLIWRCARNSRSRNLIPQAVMW 269  
QY 274 -----SHVRLERIDGSAPEFCRAVDAPAMGVSNYPGLLQNMVTHNSTIGETA 323  
Db 270 QAMDILRLIPSPVAPKDVIGNIQSGFSLKKAABSEFEI-----PEIVATFRKKNRKNEMI 325  
QY 324 NESLGATASRLSELDPSMRQRTGLATYLHNNPD-KSNVSLTA--ADPSTSV---MLSS 379  
Db 326 KESLQ-----NTIGQSLLSLMAETVSESTIDRYMSS 359  
QY 380 WAKVGLWDYDFGLGKPETV---RRPIFEPVESLMYFMPKPKPDGEFCAALSIRDEMDR 436  
Db 360 WCRKPFYVDF--GSGSPVWVGYSHTIYDNNVGVVLIDSKEGDG-VEAWISLPEDMSV 416  
QY 437 LKADKEWTKYA 447  
Db 417 FVDDQELLAYA 427

RESULT 14  
T48479  
hypothetical protein T28J14.20 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48479  
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24493  
A;Accession: T48479  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-450 <BEV>  
A;Cross-references: UNIPROT:O9LYO7; EMBL:AL163652  
A;Experimental source: cultivar Columbia; BAC clone T28J14  
C;Genetics:  
A;Map position: 5  
A;Introns: 214/1  
A;Note: T28J14.20

Query Match		5.3%; Score 124.5; DB 2; Length 450;
Best Local Similarity		19.0%; Pred. No. 0.13;
Matches		88; Conservative 71; Mismatches 190; Indels 113; Gaps 16;
QY	5	IOLDTLGQLPGLLSIYTOISLLYPVSDSQYPIVSTFEQGLKRFSEAVPW---VAGQV- 60
DB	33	LSLSTLNDPYLETLAKTIYVAPPSPNDVHDPASLFOQAL---SDALVYYVPLAGRUH 89
QY	61	-----KARGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGRKAGYP 107
DB	90	RGSHDRLRLRCSPASGV-----PFVRATADCTLSSNLKLD----- 126
QY	108	MAWFENIITAPKTLPIGCTGDDPKPVILLQNLFIKGLLITVNGHGAMDMVQDAV 167
DB	127	---MDTDLX---QLVPCDVAAPSGDYNPLALQITLFPACGGLTLATLSHSLCDGFGASQF 180
QY	168	IRLLSKACRNDPTEBEEMTAMNLDRTKIYVYLE-----NYTIGPEVDHQIVKADVAGG 220
DB	181	FKTLTE-----LAAGKTQPSIIPVMDRHLRTSNNSLNDQVBEQAPKLVDFG 228
QY	221	DAVLTQVSAWFAFFTSFKAMSEL-----KDAATKILDASTKTFVSTDDALSAPFIWKSASRV 276
DB	229	EAC---SSAATSPYTPSNDMVCEILNVTSEDTQLKEKVGAVVVTILEILAAHVWRAR--- 282
QY	277	RLERIDGSAPTFCRAVDARP-----AMGVSNVNYPGLLQNMVYHNSTI-----G 320
DB	283	-----CRALKLSPDQTSFLFGMAVGIRRIVEPPLPEGYGNAPVKANVAMKAG 329
QY	321	ETANESLGATASRLSELDPASMRQTRGLATYLLHNNPKDSNVSLTADADPSTSVMLSSW 380
DB	330	ELSNPSLHVVLKEAKKAA---QEKRYVLEQLRETEKTLKNNVACEGGKGAFMLLTDM 386
QY	381	AKVGLWD-YDFGLGLGKPTVRRPIPEPVESLMYFMPKKPDG 421
DB	387	RQGLLDEIDFGVGSVNIIPLVPKYLP--DICIFLPRKGG 426
RESULT 15		
anthranilate N-benzoyltransferase (EC 2.3.1.144) (clone pchbtl) - clove pink		
N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase		
C:Species: Dianthus caryophyllus (Clove pink)		
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004		
C:Accession: T10717		
R:Yang, Q.; Reinhard, K.; Schiltz, E.; Matern, U.		
Plant Mol. Biol. 35, 777-789, 1997		
A:Title: Characterization and heterologous expression of hydroxycinnamoyl/ benzoyl-CoA:anthranilate N-benzoyltransferase		
A:Reference number: Z17095; MUID:98088004; PMID:9426598		
A:Accession: T10717		
A>Status: preliminary; translated from GB/EMBL/DBJ		
A:Molecule type: mRNA		
A:Residues: 1-445 <YAN>		
A:Cross-references: UNIPROT:O24645; EMBL:284383; NID:g2239082; PIDN:CAB06427.1; PID:g223		
C:Function:		
A:Description: catalyzes the synthesis of anthranilate		
A:Pathway: phytoalexin biosynthesis		
C:Keywords: acyltransferase; coenzyme A		
Query Match		5.3%; Score 124; DB 2; Length 445;
Best Local Similarity		19.6%; Pred. No. 0.13;
Matches		93; Conservative 79; Mismatches 176; Indels 126; Gaps 23;
QY	20	YTOISLLYPVSDSQ---YPTIVSTFEQGLKRFSEAVPW---VAGQVKAEG---ISE 67
DB	37	HTGAVLIYKQPDNNEIHPSSSMYFDANILTEALSALVPFPYPMAGRLKINGDRYEIDC 96
QY	68	GNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGRKAGYPMAFMFENIITAPKTLPIGPG 127
DB	97	NAEGALFV---EAESHVLEDFGDF--FRPNDE-LHRVMVPTCDYSKGI----- 138
QY	128	TGPDDEPKVILLQL-NFIKGLLITVNGHGAMDMVG-----QDAV 167

Db	139	-----SSFPLIMVQLTRFCGGVSGISGPAQHVVCDGMAHFEFNNSWARIAKGLLPALPEVH 194
QY	168	IRLLSKACRNDPTEBEEMTAMNLDRTKIYVYLENYTIGPEVDHQIVKADVAGDAVLTPV 227
DB	195	DRYLHLRPNPP---QIKYSHSQPEFPVPSLPNELLDGK-----T 231
QY	228	SASWAFPTSPKAMSELKDAATKTLDAS---TKFVSTDDALSAPFIWKSASRVRLERIDGSA 285
DB	232	NKSQTLFILSRQINTLK---QKLDLSNNTTRLSTYEVVAHVWRSVSKAR--GLSDHE 285
QY	286	PTEFCRAVDARPAM---GVSNVNYPGLLQNMVYHNSTIGIEANESLGATASR----- 333
DB	286	EIKLIMPVDGRSRINNPSPKGYCGNVVFLAVCTATVGOLSCNPLTDTAGKVOEALKGLD 345
QY	334	---LRSELDPASMRQTRGLATYLLHNNPKDSNVSLTADADPSTSVMLSSWAKVGLWDYDF 390
DB	346	DDYLSAIDHTESKP---GLPVPMGSPKTYL-----PNVLVNSWGRIPYQAMDF 393
QY	391	GLGLGKPTVRRPIPEPVESLMY-----FMPKKP-DGEFCAALSRLDEMDRLK 438
DB	394	GWG-----SPTFFGISNIFYDQCFLIPSRDGDGSMTLAINLFPSSHLRPFK 439

Search completed: January 23, 2005, 19:49:36  
Job time : 31 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2005, 17:48:28 ; Search time 85 Seconds  
(without alignments)  
1903.375 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAPKIQDITGLQPLLSIY.....EDMDRLKADKWTYQAYVG 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_23Sep04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	3 AAB03935	Aab03935 Trichothe
2	2334	100.0	451	8 ADN37286	Adn37286 Trichothe
3	2314	99.1	451	3 AAY51848	Aay51848 F. gramin
4	1860.5	79.7	459	3 AAB03934	Aab03934 Trichothe
5	962.5	41.2	474	3 AAB03936	Aab03936 Sequence
6	356.5	15.3	480	7 ADE81195	Ade81195 Orf11, SE
7	175	7.5	439	8 ADO70367	Ado70367 Barley ag
8	170.5	7.3	424	3 AAG18711	Aag18711 Arabidops
9	170.5	7.3	433	3 AAG18710	Aag18710 Arabidops
10	170.5	7.3	433	8 ADO70389	Ado70389 Unidentif
11	170.5	7.3	436	6 ABUS8179	Abu58179 Wheat str
12	170.5	7.3	450	3 AAG18709	Aag18709 Arabidops
13	169.5	7.3	424	3 AAG48446	Aag48446 Arabidops
14	169.5	7.3	433	3 AAG48445	Aag48445 Arabidops
15	169.5	7.3	433	5 ABB93749	Abb93749 Herbicida
16	169.5	7.3	449	3 AAG48444	Aag48444 Arabidops
17	168.5	7.2	446	6 ABUS8173	Abu58173 Corn stre
18	165.5	7.1	333	8 ADO70372	Ado70372 Barley ag
19	161	6.9	439	6 ABUS8177	Abu58177 Soybean s
20	158.5	6.8	353	8 ADO70385	Ado70385 Barley ag
21	157.5	6.7	353	8 ADO70369	Ado70369 Wheat par
22	156.5	6.7	442	5 ABB93641	Abb93641 Herbicida
23	154.5	6.6	431	3 AAB36457	Aab36457 Mango alc
24	154	6.6	428	3 AAG24209	Aag24209 Arabidops
25	154	6.6	440	3 AAG24208	Aag24208 Arabidops

ALIGNMENTS

RESULT 1

AAB03935

ID AAB03935 standard; protein; 451 AA.

XX AAB03935;

AC AAB03935;

XX 12-SEP-2003 (revised)

DT 26-FEB-2001 (first entry)

XX Trichothecene resistance polypeptide.

XX Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;

KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.

XX Gibberella zeae.

XX WO2000060061-A2.

XX 12-OCT-2000.

XX 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

(NOVS ) NOVARTIS AG.

(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.

XX N-PSDB; AAA54209.

Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity.

Claim 15; Page 49-50; 62pp; English.

A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. (Updated on 12-SEP-2003 to standardise OS field)



Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420

Qy 421 GEFCALSLRDEDMRLKADKWKTKYAQYVG 451

Db 421 GEFCALSLRDEDMRLKADKWKTKYAQYVG 451

RESULT 3

AA51848

ID AAY51848 standard; protein; 451 AA.

XX AAY51848;

XX

DT 12-SEP-2003 (revised)

DT 09-JUN-2000 (first entry)

XX

DE F. graminearum trichothecene 3-O-acetyltransferase protein.

XX

KW Trichothecene 3-O-acetyltransferase; selective marker.

XX

OS Gibberella zeae.

XX

PN JP2000032985-A.

XX

PD 02-FEB-2000.

XX

XX 15-JUL-1998; 98JP-00200280.

XX

PR 15-JUL-1998; 98JP-00200280.

XX

PA (RIKA ) RIKAGAKU KENKYUSHO.

PA (YAMA/) YAMAGUCHI I.

XX

XX WPI; 2000-274037/24.

DR N-PSDB; AAY51848.

XX

PT Trichothecin 3-O-acetyltransferase gene useful as a selective marker in

PT gene manipulations in eukaryotic host cells.

XX

PS Claim 1a; Page 18-19; 25pp; Japanese.

XX

CC This invention describes a novel protein with trichothecin 3-O-

CC acetyltransferase activity. The gene is used as a selective marker in a

CC gene manipulation using eukaryote as the host cell. This sequence

CC represents the trichothecin 3-O-acetyltransferase isolated from Fusarium

CC graminearum. (Updated on 12-SEP-2003 to standardise OS field)

XX

SQ Sequence 451 AA;

Query Match 99.1%; Score 2314; DB 3; Length 451;

Best Local Similarity 99.1%; Pred. No. 9e-212;

Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAFKIQLDTLQGLPGLLSIYTOISLVPVSDSSQYPTIVSTFEOGLKRFSEAVPWAGQV 60

Db 1 MAFKIQLDTLQGLPGLLSIYTOISLVPVSDSSQYPTIVSTFEOGLKRFSEAVPWAGQV 60

Qy 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120

Db 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120

Qy 121 TLPFGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180

Db 121 TLPFGGTGPDPPKPVILLQNLFIKGLLITVNGQHGAMDMVQGDVAVIRLLSKACRNDPF 180

Qy 181 TEEEMTAMNLDRTIYVPLENTYIGPEVDHIOIKADVAGGDVLTTPVSASWAFFTSPKA 240

Db 181 TEEEMTAMNLDRTIYVPLENTYIGPEVDHIOIKADVAGGDVLTTPVSASWAFFTSPKA 240

Qy 241 MSELKDAATKLTLDASTKFFVSTDDALSAFTWKSASRVRLERIDGSAFTFCRAVDARPMG 300

Db 241 MSELKDAATKLTLDASTKFFVSTDDALSAFTWKSASRVRLERIDGSAFTFCRAVDARPMG 300

Qy 301 VSNYPGLLQNMTHYHNSTTIGETIANESIGATASDLRSELDPASMRQRTGLATYILHNNDK 360

Db 301 VSNYPGLLQNMTHYHNSTTIGETIANESIGATASDLRSELDPASMRQRTGLATYILHNNDK 360

Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420

Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420

Qy 421 GEFCALSLRDEDMRLKADKWKTKYAQYVG 451

Db 421 GEFCALSLRDEDMRLKADKWKTKYAQYVG 451

RESULT 4

AA803934

ID AAB03934 standard; protein; 459 AA.

XX AAB03934;

XX

DT 26-FEB-2001 (first entry)

XX

DE Trichothecene resistance polypeptide.

XX

KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;

KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.

XX

OS Fusarium sporotrichioides.

XX

PN WO2000060061-A2.

XX

PD 12-OCT-2000.

XX

XX 29-MAR-2000; 2000WO-EP002769.

PF 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX

XX (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX

XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

PI WPI; 2000-679374/66.

DR N-PSDB; AAA54206.

XX

PT Plant cell for preventing mycotoxin contamination of wheat, maize, barley

PT or rice plant, comprises heterologous polynucleotide encoding gene

PT product expressed in cell, having trichothecene resistance activity.

XX

PS Claim 15; Page 46-48; 62pp; English.

XX

CC A heterologous gene encoding a gene product which confers trichothecene

CC resistance can be used to transform plant cells to make them resistant to

CC fungal infection. The transformation method is useful for preventing

CC mycotoxin contamination of a plant, particularly a crop plant such as

CC wheat, maize, barley or rice, and for reducing and/or preventing the

CC growth of a fungus of the genus Fusarium that produces a trichothecene,

CC preferably comprising a C-3 hydroxyl group, by growing transformed crop

CC plants in an area which is moderate to severe fungal infestation

XX

SQ Sequence 459 AA;

Query Match 79.7%; Score 1860.5; DB 3; Length 459;

Best Local Similarity 77.6%; Pred. No. 2e-168;

Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

Qy 2 AFKIQLDTLQGLPGLLSIYTOISLVPVSDSSQYPTIVSTFEOGLKRFSEAVPWAGQV 61

Db 11 SFDIELDIICQOPPLLSIYTOISLVPVSDPSQYPTIVSTLBEGLKRLSQTFFPWAGQV 70

Qy 62 AEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 121

Db 71 TEGISEGNTGTSKIIIPYEETPLRLVKDLRDDSSAPTIEGLRKAGFPLEMFENVAPRK 130



QY 122 LPTGCTGDDPKPVILLQILNFKIGGLILTVNGHGMVGDVIRLLSKACRNDPFT 181  
 Db 131 LAIGPENGNDPKPVILLQILNFKIGGLILTVNGHGMVGDVIRLLSKACRNEST 190  
 QY 182 EBEAMNLDKRTIVPYLNYTIGPVDHQIVKADVAGDAVLTPVSAWAFPTFSPKAM 241  
 Db 191 EBEISAMNLDKRTIVPYLNYTIGPVDHQIVKADVAGDAVLTPVSAWAFPTFSPKAL 249  
 QY 242 SELKDAATKTLDASTFKVSTDDALSFAFIWKSASRVRLERIDGSAPTEFCRAVDARPMGV 301  
 Db 250 SELKDAATKTLDASSFKVSTDDALSFAFIWQSTSRVRLARLDASTPTFCRAVDMRGPVG 309  
 QY 302 SNYPGLLQNTVYHSTIGEIANESIGATASRLRSELDPASRQRTGLATYLNHPDKS 361  
 Db 310 SSTYPGLLQNTVYHSTIGEIANESIGATASRLRSELDPASRQRTGLATYLNHPDKS 369  
 QY 362 NVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPEVTRRPIFEVPEVSLMYFMPKPPDG 421  
 Db 370 SVSLTADANPSSIMLSSWAKVGCWEYDFGLGKPEVTRRPIFEVPEVSLMYFMPKPPDG 429  
 QY 422 EFCALSLRDEMDRLKADKWTYKAYQYVG 451  
 Db 430 EFTASISLRDEMDRLKADKWTYKAYQYVG 459

RESULT 5  
 AAB03936  
 ID AAB03936 standard; protein; 474 AA.

AC AAB03936;  
 XX

DT 26-FEB-2001 (first entry)

Sequence encoding trichothecene resistance polypeptide.

DE Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;  
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.  
 XX Saccharomyces cerevisiae.

XX WO2000060061-A2.

PD 12-OCT-2000.

PF 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hohn TM, Peters C, Salmerton JM, Reed JN, Dawson JL;  
 PI

XX WPI; 2000-679374/66.

DR N-PSDB; AAA54210.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
 PT or rice plant, comprises heterologous polynucleotide encoding gene  
 PT product expressed in cell, having tricothecene resistance activity.

XX Claim 15; Page 51-52; 62pp; English.

XX A heterologous gene encoding a gene product which confers tricothecene  
 CC resistance can be used to transform plant cells to make them resistant to  
 CC fungal infection. The transformation method is useful for preventing  
 CC mycotoxin contamination of a plant, particularly a crop plant such as  
 CC wheat, maize, barley or rice, and for reducing and/or preventing the  
 CC growth of a fungus of the genus Fusarium that produces a tricothecene,  
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop  
 CC plants in an area which is moderate to severe fungal infestation

SQ Sequence 474 AA;

Query Match 41.2%; Score 962.5; DB 3; Length 474;  
 Best Local Similarity 44.4%; Pred. No. 1.4e-82;  
 Matches 202; Conservative 84; Mismatches 156; Indels 11; Gaps 8;

QY 6 QLDTLGQLPGLLSIYTOISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQVKABGI 65  
 Db 22 QLDILGQPSLYKLYQCSIVRVPDPSAHDHIVNTLRTGLETLAKNFQWLAGNVVNEGA 81  
 QY 66 SSGNTGTSTFIVPFEDVPRVVKDLDDPSAPTEIEGRKAGYPMAMFENIAPKTL-PI 124  
 Db 82 DEGNTGTYRIIVPSDKIP-LIVQDLREDSAPTMDSLEKADPEIYMLDEKTFAPCMTINPP 140  
 QY 125 GPGTG-PDDPKPVILLQILNFKIGGLILTVNGHGMVGDVIRLLSKACRNDPFTTEE 183  
 Db 141 GNTIGMAAKSGPVFAVQANFISGGVLVTVGOHNMIDITGQESIINLNKSCHQKPFSD 200  
 QY 184 EMTANMLDKRTIVPYLNYTIGPEVD--HQIVKA--DVAGGDAVLTPVS-ASWAFPTFSP 238  
 Db 201 ELLIGNIDKSKSIPLFDE-TWEPDITLVHEIVETSRNTSGEKEQSCSSNSTWAVVEFSA 259  
 QY 239 KAMSELKDAATKTLDASTFKVSTDDALSFAFIWKSASRVRLERIDGSAPTEFCRAVDARPA 298  
 Db 260 ISLQNLRIILAMQTCSTGTFKPVSTDDITVAFIWKSVSRARLSKLPETKSNLGRAVDVRKR 319  
 QY 299 MGVSNYPGLLQNTVYHSTIGEIANESIGATASRLRSELDPA--SMRQRTGLATYLNH 356  
 Db 320 LGLPETYPGLLVNMTFTGSLKSLDKSLGVLASQIRKLDPKVPDLAVNTCALATLLSR 379  
 QY 357 NPKNSVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPEVTRRPIFEVPEVSLMYFMP 416  
 Db 380 CPDKTKVSIQPIDTLTSGIMVSSWAKVSLYDVFNLGLGKPKSVRRPRFISLESIIYFMP 439  
 QY 417 KKPDEGFCALSLRDEMDRLKADKWTYKAYQYVG 451  
 Db 440 RSSRGGMVVALCLRDQWECNLNADKEWNTYATHIG 474

RESULT 6

ADE81195  
 ID ADE81195 standard; protein; 480 AA.

AC ADE81195;

DT 29-JAN-2004 (first entry)

XX Orf11, SEQ ID 23.

XX ML-236B; HMG-CoA reducing enzyme; Orf11.

OS Penicillium citrinum.

XX JP2003116567-A.

XX 22-APR-2003.

XX 15-OCT-2001; 2001JP-00316578.

XX 15-OCT-2001; 2001JP-00316578.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2003-817677/77.

XX N-PSDB; ADE81194.

XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-  
 PT 236B production in ML-236B producing microbe.

XX Example 8; SEQ ID NO 23; 142pp; Japanese.

XX The present invention relates to a DNA sequence (I, ADE81173), which is  
 CC associated with ML-236B synthesis. (I) is useful for improving ML-236B

CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing  
 XX microbe. The present sequence was used to illustrate the invention.  
 SQ Sequence 480 AA;

Query Match 15.3%; Score 356.5; DB 7; Length 480;  
 Best Local Similarity 26.5%; Pred. No. 1.2e-24;  
 Matches 129; Conservative 87; Mismatches 183; Indels 87; Gaps 20;

QY 25 LLYPVSDSSQYPTVTFEQLKRFSEAVPWAG---QVKAEGISEGNTGTSTFV---PF 78  
 DB 20 LCFPHSDAS-IPQTVSVLRGLSKVYAKLLFLGNLQVENAGLRFG---SPAVESNFS 74  
 QY 79 EDVPRVVVKDLRDDPSAP---TIEGRKAGYPMWMDENIIPRKLPIGPGTGDPPDKP 135  
 DB 75 EP-PTLSVRDMSGSDTWSWTYHDLRERGFPMSLNLDVLP-----TDPGSGRT 124  
 QY 136 VIL-LQNLFTKGLLITVNGQHGAMDMGDVIRLLSKACRNDPTEDEM-----185  
 DB 125 RLIAQAQNFIPGGLLYVSTSHAFAGFLSTLCEWSQCRDALGTSDEIPNVSKQEI 184  
 QY 186 -TAMNLD---RTIV-PYLENYTIGPEVDHQIVKADVAGD-----AVLTPVS 228  
 DB 185 STALDQDSPCRSLVQPYSPTSVAYERLKSPILMHVLGLDWRPKERSRILMSQIPSP 244  
 QY 229 ASWAFTEPKAMSELKDA---TKTLDASTKPVSTDDALSATFKWSASRVRL-ERIDGS 284  
 DB 245 VRSCIFSIANSVEKLQVALGSSGVPKSSQSISTDALGALLSCLMRARLTERESFE 304  
 QY 285 APTF--FCRAVDARPAMGVSNNYPG-----LLQNTYHNSITGIEIANESLG 328  
 DB 305 NPKAETMARVAVNVRKLLSVPEHLGNTILYAVTKLSIDLATRGTDHLNVVAQSLRESL- 363  
 QY 329 ATASRLRSELDPASMRQRTGLATYLHNPNPKSNVSLTADADPSTSVMLSSWAKVGLWDY 388  
 DB 364 -----DELKSSMQEAVELA---NNIPDVGRMGSLSPFTWVAENWVSSLSRLPLDW 413  
 QY 389 DFGL-----GLGKETVRRPIFEVSLMYPMKPGDFCAALSDREDDMDRLKADKEWT 444  
 DB 414 DFGSISHGGLGKPDNRFP-DKCFEGITFTMPQPDGSLIEMITMKAVDMELMTDQTF 472  
 QY 445 KYAQYV 450  
 DB 473 EFPFV 478

RESULT 7  
 ADO70367  
 AC ADO70367 standard; protein; 439 AA.  
 XX  
 AC ADO70367;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Barley agmatine coumaroyltransferase.  
 XX  
 KW barley; agmatine coumaroyltransferase; ACT; antimicrobial;  
 KW pathogen resistance; enzyme.  
 XX  
 OS Hordeum vulgare.  
 XX  
 PN WO2004044195-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 11-NOV-2003; 2003WO-EP012601.  
 XX  
 PR 12-NOV-2002; 2002EP-00025076.  
 XX  
 PA (RISO-) RISO NAT LAB.  
 XX  
 PI Rasmussen S, Burhenne K, Kristensen B;  
 XX

DR WPI; 2004-431667/40.  
 XX N-PSDB; ADO70366.  
 PT New polynucleotide encoding a polypeptide having agmatine  
 PT coumaroyltransferase (ACT) activity, useful for establishing or enhancing  
 PT a pathogen resistance in a plant, and for producing a biopolymer.  
 XX Claim 1; Fig 1; 11pp; English.  
 XX The present invention provides the protein and coding sequences of the  
 CC barley agmatine coumaroyltransferase (ACT) enzyme. The sequences are  
 CC useful for the preparation of an antimicrobial compound, its precursor or  
 CC a plant protection composition, for establishing or enhancing a pathogen  
 CC resistance in a plant, and for producing a biopolymer. The present  
 CC sequence is the protein of the invention.  
 XX Sequence 439 AA;

Query Match 7.5%; Score 175; DB 8; Length 439;  
 Best Local Similarity 23.8%; Pred. No. 2.3e-07;  
 Matches 118; Conservative 62; Mismatches 185; Indels 130; Gaps 26;

QY 2 AFKIQDLDTLGLQPLGLLSIVTOISLLVPVSDSSQYPTIVS-----TFEQGLKR 48  
 DB 10 AVKPEVGACGLAPGCTADVPLITVL-----DKANFTYISVIYAFHAPAPNAVLEAGLR 65  
 QY 49 -FSEAVPWVAGQ--VKAEG---ISEGNTGTSTFVPEFEDVPRVVVKDLRDDPSAPTEGMR 102  
 DB 66 ALVDYREM-AGRLGVDSAGGRAILLNDAGARFVEATADVALDSVMPLK-----PTSE--- 116  
 QY 103 KAGYPMWMDENIIPRKLPIGPGTGDPPDKPVILLQL-NFKKGLLITVNGQHGAMDM 161  
 DB 117 -----VLSLHP-SGDDGPEELMLIQVTFACGSLVGVFTTQHIVSDG 157  
 QY 162 VGODAVIRELLSKACRN---DP-----FTEEMTANMLDRKTI--VPYLENYTIGPE 207  
 DB 158 RTGNTFFVAMSOATRGALIDPVVHDRAFFHPREPLHVEYHRGVEFPY-----E 209  
 QY 208 VDHQIV-KADVAGGDAVLTPVSASWAFTFSPKAMSELKDAATKTLDASTKPVSTDDALS 266  
 DB 210 KAHDVVGADGDEDEVVNVKH-----FSREFISKKAQASA---GAPRPCSTLQCVV 259  
 QY 267 AFIKWSASRVRLERIDGSAPTEFCRAVDARPAMG--VSNNYPGLLQNTYHNSITGIEI-- 322  
 DB 260 AHLWRSMTWAR--GLDGGETTVAIAVDGRARMSQVDPDGTGNVILWARPPTTAGELVT 317  
 QY 323 -----ANESIGATASRL-----RSELDPASMRQRTGLATYLHNPNPKSNVSLTADADP- 371  
 DB 318 RPVKHAVELISREVARINDGYKSFIDFAN-----SGAVEKERLVATADADM 365  
 QY 372 --STSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIF-----EPVESLMTYMPK-KPDGEF 423  
 DB 366 VLSPNIEVDSWLLIPFYDMDFGG-----RPFPMPSYLPVEGLILLPSFLGDSV 417  
 QY 424 CAALSRLDEDMRLK 438  
 DB 418 DAYVPLFSRDMNTFK 432

RESULT 8  
 AAG18711  
 ID AAG18711 standard; protein; 424 AA.  
 XX  
 AC AAG18711;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 20229.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX



PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
PR	22-SEP-1999;	99US-0155139P.	
PR	23-SEP-1999;	99US-0155486P.	
PR	24-SEP-1999;	99US-0155659P.	
PR	28-SEP-1999;	99US-0156458P.	
PR	29-SEP-1999;	99US-0156596P.	
PR	04-OCT-1999;	99US-0157117P.	
PR	05-OCT-1999;	99US-0157753P.	
PR	06-OCT-1999;	99US-0157865P.	
PR	07-OCT-1999;	99US-0158029P.	
PR	08-OCT-1999;	99US-0158232P.	
PR	12-OCT-1999;	99US-0158369P.	
PR	13-OCT-1999;	99US-0159293P.	
PR	13-OCT-1999;	99US-0159295P.	
PR	14-OCT-1999;	99US-0159329P.	
PR	14-OCT-1999;	99US-0159330P.	
PR	14-OCT-1999;	99US-0159331P.	
PR	14-OCT-1999;	99US-0159637P.	
PR	18-OCT-1999;	99US-0159638P.	
PR	21-OCT-1999;	99US-0159584P.	
PR	21-OCT-1999;	99US-0160741P.	
PR	21-OCT-1999;	99US-0160767P.	
PR	21-OCT-1999;	99US-0160768P.	
PR	21-OCT-1999;	99US-0160770P.	
PR	21-OCT-1999;	99US-0160814P.	
PR	21-OCT-1999;	99US-0160815P.	
PR	22-OCT-1999;	99US-0160980P.	
PR	22-OCT-1999;	99US-0160981P.	
PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161406P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
PR	26-OCT-1999;	99US-0161320P.	
PR	28-OCT-1999;	99US-0161992P.	
PR	28-OCT-1999;	99US-0161993P.	
PR	29-OCT-1999;	99US-0162142P.	
<div>Query Match Best Local Similarity 7.3%; Score 170.5; DB 3; Length 424; Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;</div>			
QY	36	PTIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSFIYPPFEDVPRV 84	
DB	35	PTGASNFFDPQVNMKEALSALVFYPMAGRLKRDGDDGRIEIDCNGAGVLFVW--ADTPSV 92	
QY	85	VVKDLRDD--PSAPTEGMRKAGYPWAMFDENIIAPRKLTP-IGPGTGDDPKPVLLOL 141	
DB	93	I-----DDFGDAPT-----NU-----RQLPEVDHSTGIHS-FPLLVLQV 128	
QY	142	NFTK-GGLILTNGQHGAMVQGDVIRLLSKACRNDPTEEMTAMNLDRTIYVYLE 200	
DB	129	TFPKCGASLGVGMHAAADGFGSLHFIWSDMAR-----GLD----- 167	
QY	201	NTTIGEVVDHIVKA-----DVAGGDAVLTPVSASWAFTFSPKAM 241	
DB	168	-LTIPFIDRTLRLARDPPQPAFHVEYQAPSMKIPLDPSKSGPENTTVSIFKLTRDQL 226	
QY	242	SELKDAATKTLDASTKFVSTDDALSAPFVKSASRVRLERIDGSAPEFCRAVDA----RP 297	
DB	227	VALK--AKSKEDGNTVSYSEYMLAGHVRSVCKAR--GLPNDQETKLIATDGRSLRP 282	
QY	298	AMGVSNYFCLLQNMTHNSTI-----GEIANESLGATASRLRSELDPAS 342	
DB	283	QLP-----FGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLSALD--- 334	
QY	343	MRQRTGLATYLNHPDKNSVLTADPSTSVMLSSWAKVGLWYDFGLGCKPQTVTR 402	

Db	335	-----YLEMQPDLALVRGAHTYKCPNLGITSWRLPIYDADFGWG-----R 376
QY	403	PIPE-----PVRSLMYFMPKPKP-DGEFCAALSRLRDEDM 434
DB	377	PIFMGPGGIPYEGLSFVLPSPNTDNGSLSLVAIALQSEHM 414
RESULT 9		
AAAG18710		
ID	AAAG18710 standard; protein; 433 AA.	
XX	AAAG18710;	
XX	17-OCT-2000 (first entry)	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 20228.	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PD	06-SEP-2000.	
PF	25-FEB-2000; 2000EP-00301439.	
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	23-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	28-APR-1999;	99US-0130891P.
PR	28-APR-1999;	99US-0131449P.
PR	30-APR-1999;	99US-0132048P.
PR	30-APR-1999;	99US-0132407P.
PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	07-MAY-1999;	99US-0132487P.
PR	11-MAY-1999;	99US-0132863P.
PR	14-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138847P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.

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PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142377P.
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Query Match 7.3%; Score 170.5; DB 3; Length 433;
Best Local Similarity 23.4%; Pred. No. 6e-07;
Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;
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Db 44 PTGASNFDPQVMKEALSKALVPFPYPMAGRLKRDGRIEIDCNGAGLVFVV--ADTPSV 101
QY 85 VVKLRDD--PSAPTIEGMRKAGYPMAMFDENIIAPRKTLP-IGGTGTPDDPKPVILLQL 141
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Db 102 i-----DDFGDFAPTL-----NL-----QLIPEVDHSTGIHS-FPLLVLQV 137  
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 Db 138 TPFKCGGASLGVGMQHAADGFGSLHFINTWSDMAR-----GLD----- 176  
 QY 201 NYTIGEVHDIQVKA-----DVAGGDAVLTPVSASWAFTEFSPKAM 241  
 Db 177 -LTIPFDITLRLARDPPQPAFHVEYQAPSMKIPDPSKSGPENTTVSIFKLRDQL 235  
 QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVLERIDGSAPEFCRAVDA-----RP 297  
 Db 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSRLRP 291  
 QY 298 AMGVSNNYPGLLQNMTHYHNSI-----GEIANESLGATASRLRSELDPAS 342  
 Db 292 QLP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLSALD--- 343  
 QY 343 MRQRTGLATYLNHNPDKNSVLTADAPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRR 402  
 Db 344 -----YLEMQPDLGALVRGAHTYKCPNLGITSWVRLPYDADFGWG-----R 385  
 QY 403 PIPE-----PVESLMYFMPKPK-DGEFCAALSRLRDEDM 434  
 Db 386 PIFMGPGGIPYEGLSFVLPSPTNDGSLSVAILQSEHM 423  
 RESULT 10  
 ADO70389  
 ID ADO70389 standard; protein; 433 AA.  
 XX  
 AC ADO70389;  
 DT 12-AUG-2004 (first entry)  
 DE Unidentified plant transferase #3.  
 XX  
 KW plant; transferase; ACT; antimicrobial; pathogen resistance; enzyme;  
 KW agmatine coumaroyltransferase.  
 XX  
 OS Viridiplantae.  
 XX  
 PN WO2004044195-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 11-NOV-2003; 2003WO-EP012601.  
 XX  
 PR 12-NOV-2002; 2002EP-00025076.  
 XX  
 PA (RISO-) RISO NAT LAB.  
 XX  
 PI Rasmussem S, Burhenne K, Kristensen B;  
 XX  
 DR WPI; 2004-431667/40.  
 XX  
 PT New polynucleotide encoding a polypeptide having agmatine  
 PT coumaroyltransferase (ACT) activity, useful for establishing or enhancing  
 PT a pathogen resistance in a plant, and for producing a biopolymer.  
 XX  
 PS Disclosure; Fig 6; ilpp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of the  
 CC barley agmatine coumaroyltransferase (ACT) enzyme. The sequences are  
 CC useful for the preparation of an antimicrobial compound, its precursor or  
 CC a plant protection composition, for establishing or enhancing a pathogen  
 CC resistance in a plant, and for producing a biopolymer. The present  
 CC sequence is a transferase sequence used in a homology comparison with the  
 CC sequence of the invention.  
 XX  
 SQ Sequence 433 AA;

Query Match 7.3%; Score 170.5; DB 8; Length 433;  
 Best Local Similarity 23.4%; Pred. No. 6e-07;  
 Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;  
 QY 36 PTIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG-----ISBNTGTSTFIVPFEDVPRV 84  
 Db 44 PTGASNFFDPQVMEALSALVFPFPMAGRLKRDGRIEIDCNGAGVLFVV--ADTPSV 101  
 QY 85 VVKDLRDD--PSAPTIEGMRKAGYPMAMPDENIIAPRKTL-IPGCTGDDPKPKVILLQL 141  
 Db 102 I-----DDFGDFAPTL-----NL-----QLIPEVDHSTGIHS-FPLLVLQV 137  
 QY 142 NFIK-GGLILTVNGQHGAMVQDQAVIRLLSKACRNDPTEBEMTAMNLDKRTIIVPYLE 200  
 Db 138 TPFKCGGASLGVGMQHAADGFGSLHFINTWSDMAR-----GLD----- 176  
 QY 201 NYTIGEVHDIQVKA-----DVAGGDAVLTPVSASWAFTEFSPKAM 241  
 Db 177 -LTIPFDITLRLARDPPQPAFHVEYQAPSMKIPDPSKSGPENTTVSIFKLRDQL 235  
 QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVLERIDGSAPEFCRAVDA-----RP 297  
 Db 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSRLRP 291  
 QY 298 AMGVSNNYPGLLQNMTHYHNSI-----GEIANESLGATASRLRSELDPAS 342  
 Db 292 QLP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLSALD--- 343  
 QY 343 MRQRTGLATYLNHNPDKNSVLTADAPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRR 402  
 Db 344 -----YLEMQPDLGALVRGAHTYKCPNLGITSWVRLPYDADFGWG-----R 385  
 QY 403 PIPE-----PVESLMYFMPKPK-DGEFCAALSRLRDEDM 434  
 Db 386 PIFMGPGGIPYEGLSFVLPSPTNDGSLSVAILQSEHM 423  
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 ABUS8179  
 ID ABUS8179 standard; protein; 436 AA.  
 XX  
 AC ABUS8179;  
 DT 14-APR-2003 (first entry)  
 DE Wheat stress response protein #7.  
 XX  
 KW Plant; EST; expressed sequence tag; stress response; drought; heat;  
 KW radiation; pathogen attack; grain flavour; disease resistance;  
 KW peptide-methionine sulphoxide reductase; DNA repair; enzyme;  
 KW intracellular protein transport.  
 XX  
 OS Triticum aestivum.  
 XX  
 PN US2002152497-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 19-FEB-2002; 2002US-00078929.  
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 PR 11-MAY-1999; 99US-0133437P.  
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 PR 05-MAY-2000; 2000US-00566394.  
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 PA (FAMO/) FAMODU O O.  
 PA (MEYE/) MEYERS B C.





PR 18-JUN-1999; 99US-0139456P.  
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Query Match 7.3%; Score 170.5; DB 3; Length 450;

Best Local Similarity 23.4%; Pred. No. 6.4e-07;

Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

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QY 85 VVKDLRDD--PSAPTTEGKRGAGYPMAMFDENIAPRKTLF-IGPGTGPDDPKPVILLQL 141

Db 119 I-----DDEGDFAPTL-----NL---RLIPEVDHSTGIHS-FPLLVLQV 154

QY 142 NFIK-GGLILTVNGQHGAMDMVQDAVIRLLSKACRNDPFTBEETAMNLDRTIIVPYLE 200

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Qy      201  NVTIGSEVDHQIVKA-----DVAGDAVLTPVSASWAFFTFSPKAM 241
Db      194  -LTIPFIDRTLRLARDPQPAFHVEYQAPSMKIPLDPSKSGPENTTVSIFKLTRDQL 252
Qy      242  SELKDAATYLDASTKFVSTDDALSAPFIWKSASRVRLERIDGSAPEFCRAVDA---RP 297
Db      253  VALK--AKSKEDGNTVSYSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSLRP 308
Qy      298  AMGVSNNYPGLLQNMTHNSTI-----GEIANESLGATASRLRSLEDPAS 342
Db      309  QLP-----PGYGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD--- 360
Qy      343  MRQTRGLATYLNHNPDKNSVLTADAPSTSVMLSSWAKVGLWYDFGLGKPKETVWR 402
Db      361  -----YLEMQPDLGALVRGATYKCPNLGITSWVRLPIYDADFGWG-----R 402
Qy      403  PIPE-----PVESLMYFMPKKP-DGEFCAALSRLRDEDM 434
Db      403  PIFMFGGPIYEGLSFVLPSTNDGSLSVAILAQSEHM 440

RESULT 13
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XX
AC      AAG48446;
XX
DT      18-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana protein fragment SEQ ID NO: 61177.
KW      Protein identification; signal transduction pathway; metabolic pathway;
KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
XX
OS      Arabidopsis thaliana.
XX
PN      EF1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-00301439.
XX
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PR      27-MAY-1999; 99US-0136392P.
PR      28-MAY-1999; 99US-0136782P.
PR      01-JUN-1999; 99US-0137222P.
PR      01-JUN-1999; 99US-0137528P.
PR      03-JUN-1999; 99US-0137502P.
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PR      07-JUN-1999; 99US-0138094P.
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Best Local Similarity 23.0%; Pred. No. 7.2e-07;  
Matches 105; Conservative 61; Mismatches 156; Indels 135; Gaps 23;  
  
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QY 85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFEDENIAPRKTLPFGTGTGPDPPKPVILLQLN 142  
DB 93 I-----DDFGDFAPTL-----NL---RLIPEVDHAGIHSFPLLVQVT 129  
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DT 18-OCT-2000 (first entry)  
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KW termination sequence.  
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Query Match 7.3%; Score 169.5; DB 3; Length 433;
Best Local Similarity 23.0%; Pred. No. 7.4e-07; Indels 135; Gaps 23;
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DB 177 LTIPPFIDRTLRLARPPQPAPFHVEYQAPSKIPLDPSKSGPENTTVSIFKLTQDLV 236
QY 243 ELKDAATKTLDASTKFTVSTDDALSAPFIWKSASRVRLERIDGSAPTFCRAVDA-----RPA 298
DB 237 ALK--AKSKEDGNTVSYSYEMLAGHVMSVGKAR--GLPNDQETKLYIATDGRSLRPQ 292
QY 299 MGVSNNYPGLLQNMVTHNSTI-----GETANESLGATASRLSELDPSAM 343
DB 293 LP-----PGYFGNVIPTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLSALD----- 343
QY 344 RQRTGLATYLNHPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKRPETVRRP 403
DB 344 -----YLEMQPDLALSALVRGAHTYKCPNLGITSWVRLPIYDADFGWG-----RP 386
QY 404 IFE-----PVESLMYFMPKKP-DGEFCAALSURDEDM 434
DB 387 IFMGPGGIPYEGLSFVLPSPTNDGSLSAIALQSEHM 423

RESULT 15
ABB93749
ID ABB93749 standard; protein; 433 AA.
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AC ABB93749;
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DT 31-MAY-2002 (first entry)
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DE Herbicidally active polypeptide SEQ ID NO 2960.
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KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP009892.
XX
PR 28-AUG-2001; 2001WO-EP009892.
XX
PA (FARB ) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
XX WPI; 2002-269010/31.
XX
DR Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms.
XX
PS Claim 5; SEQ ID NO 2960; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
XX for herbicidally active compounds, comprising aligning and comparing
XX nucleic acid or amino acid sequences from plant with nucleic acid or
XX amino acid sequences from non-plant organisms using suitable search
XX parameters, where plant sequences having an E-value greater by a factor
XX of 3 than the E-value of most similar non-plant sequences are selected.
XX The polypeptides or nucleic acids encoding them are useful for
XX identifying modulators. The identified modulators are useful as
XX herbicides
XX
SQ Sequence 433 AA;

Query Match 7.3%; Score 169.5; DB 5; Length 433;
Best Local Similarity 23.0%; Pred. No. 7.4e-07; Indels 135; Gaps 23;
Matches 105; Conservative 61; Mismatches 156;

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QY 344 RQRTGLATYLNHPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKRPETVRRP 403
DB 344 -----YLEMQPDLALSALVRGAHTYKCPNLGITSWVRLPIYDADFGWG-----RP 386
QY 404 IFE-----PVESLMYFMPKKP-DGEFCAALSURDEDM 434
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us-10-614-954-6.rag

Wed Jan 26 11:53:58 2005

Db 387 IFMFGIFYEGLSFVLPSPPTNDGSLVAIALQSEHM 423

Search completed: January 23, 2005, 19:47:10  
Job time : 89 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 16:28:15 ; Search time 817 Seconds  
(without alignments)  
9536.627 Million cell updates/sec

Title: US-10-614-954-5  
Perfect score: 1356  
Sequence: 1 atgggttcaagatacagct.....atgcgcagctagcttggttag 1356

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
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21: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	13	US-10-074-279-5
2	1356	100.0	1356	13	US-10-614-954-5
3	915.6	67.5	1403	13	US-10-074-279-1
4	915.6	67.5	1403	16	US-10-614-954-1
5	915.6	67.5	12949	13	US-10-074-279-11
6	915.6	67.5	12949	16	US-10-614-954-11
7	915.6	67.5	13737	13	US-10-074-279-10
8	915.6	67.5	13737	16	US-10-614-954-10
9	249.8	18.4	1425	13	US-10-074-279-7
10	249.8	18.4	1425	16	US-10-614-954-7
11	146.2	10.8	695	18	US-10-653-047-4594
12	39.2	2.9	1947	15	US-10-369-493-27681

13	36.4	2.7	688	17	US-10-767-701-11710	Sequence 11710, A
14	36.2	2.7	684	17	US-10-767-701-11709	Sequence 11709, A
15	36	2.7	1707	18	US-10-425-115-66302	Sequence 66302, A
16	35.8	2.6	2463	16	US-10-320-797-7	Sequence 7, Appl
17	35.6	2.6	1459	18	US-10-363-345A-20283	Sequence 20283, A
18	35.6	2.6	1459	18	US-10-363-345A-20284	Sequence 20284, A
19	35.6	2.6	1463	18	US-10-363-345A-1033	Sequence 1033, Ap
20	35.6	2.6	1463	18	US-10-363-345A-1034	Sequence 1034, Ap
21	35.4	2.6	520	17	US-10-767-701-24625	Sequence 24625, A
22	35.4	2.6	2400	15	US-10-369-493-37751	Sequence 37751, A
23	35.2	2.6	801	17	US-10-437-963-84244	Sequence 84244, A
24	35.2	2.6	837	14	US-10-184-634-352	Sequence 352, App
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26	35	2.6	556	14	US-10-184-634-136	Sequence 136, App
27	35	2.6	556	14	US-10-184-634-136	Sequence 136, App
28	35	2.6	556	14	US-10-063-685-24	Sequence 24, Appl
29	35	2.6	2448	17	US-10-437-963-86614	Sequence 86614, A
30	34.6	2.6	427	16	US-10-374-780A-932	Sequence 932, App
31	34.6	2.6	427	16	US-10-425-115-135877	Sequence 135877, A
32	34.6	2.6	1112	13	US-10-027-632-31187	Sequence 31187, A
33	34.6	2.6	1112	13	US-10-027-632-31188	Sequence 31188, A
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37	34.2	2.5	1377	15	US-10-369-493-46533	Sequence 46533, A
38	34	2.5	1584	16	US-10-282-122A-27075	Sequence 27075, A
39	34	2.5	1770	18	US-10-411-910A-110	Sequence 110, App
40	34	2.5	3115	18	US-10-363-345A-30243	Sequence 30243, A
41	34	2.5	3115	18	US-10-363-345A-30244	Sequence 30244, A
42	33.8	2.5	26923	16	US-10-672-787-41	Sequence 41, Appl
43	33.8	2.5	322	16	US-10-242-535A-19650	Sequence 19650, A
44	33.8	2.5	322	16	US-10-085-783A-19650	Sequence 19650, A
45	33.8	2.5	549	18	US-10-425-115-111874	Sequence 111874, A
			2913	15	US-10-172-118-442	Sequence 442, App

ALIGNMENTS

RESULT 1  
US-10-074-279-5 -  
; Sequence 5, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-10-074-279-5

Query Match	100.0%	Score 1356	DB 13	Length 1356
Best Local Similarity	100.0%	Pred. No. 0		
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Db	1	ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGGCTCTCTTCGATCTAC	60	
QY	61	ACCAAAATCAGTCTCTCTTACCCCGCTCTGTGATTCCTCTCAATATCCCACTATTGTGAGC	120	



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QY 241 GTTCTCTGTGTTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGGT 300  
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QY 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGGAGAAACATCATCGCCCAAGGAAG 360  
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Db 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGT 660  
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RESULT 2  
US-10-614-954-5  
; Sequence 5, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dilli-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-10-614-954-5  
Query Match 100.0%; Score 1356; DB 16; Length 1356;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 481 ATGGTAGGCAAGATCGCGGTGATCGCTCTACTCTCCAAAGCGGTGCGTAACGACCCATTTC 540  
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Qy 841 ATCGATGGCTCTGACCTACCGAGTTCTCGCGTCTGTTGATGCTCGACCGGCAATGGGT 900  
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Db 1081 TCAACGATATCCCTGACGCTGATGCGGACCACTTACCAAGCTCATGCTGAGTCTTGG 1140  
Qy 1141 GCCAAGTGGGACTCTGGGATTAACGATTTGGGCTCGGACCTTACCAAGCTCATGCTG 1200  
Db 1141 GCCAAGTGGGACTCTGGGATTAACGATTTGGGCTCGGACCTTACCAAGCTCATGCTG 1200  
Qy 1201 AGACGCGCAATCTTTCAGCTGTTGAGAGCTTGTATGCTTTATGCCCAGAGCTGAT 1260  
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Db 1261 GCGAGTCTTGTGCGGCGCTTCTCTGAGGATGAGGATATGACCGATTTGAAGGCGGAT 1320  
Qy 1321 AAGGAGTGACCAAGTATGCGGAGTACGTTGGTTAG 1356  
Db 1321 AAGGAGTGACCAAGTATGCGGAGTACGTTGGTTAG 1356

## RESULT 3

US-10-074-279-1  
; Sequence 1, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1403  
; TYPE: DNA  
; ORGANISM: Fusarium sporotrichioides  
; US-10-074-279-1

Query Match 67.5%; Score 915.6; DB 13; Length 1403;

Best Local Similarity 80.3%; Pred. No. 2.6e-306;

Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

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Qy	123	CTTCGAGCAAGGTCTTAAGCGTCTTCCGAAGCGTCTCCATGCGTCCAGTCCAGGCCAGGTCAA	182
Db	156	CCTTGAGGAGGCCCTTAAACCGCTCTCTCAAACTCTTCCATGGGTCGCGGCCAGGTCAA	215
Qy	183	AGCCGAGGSCATTAGCGAGGAAACACAGCAACTCTCTTTATCGTCCCTTTTCAGGACGT	242
Db	216	GACCGAGGSCATCAGCGAAGAAACACAGCAACTTCCAAGATCATTCATATGAGGAGAC	275
Qy	243	TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCAGCGCCCAACGATCGAGGATAT	302
Db	276	ACCCCGTCTTGTGTGAAGACCTCGTGTATGATTCCTCAGCGCCCAACGATCGAGGAT	335
Qy	303	GAGAAAGCGGATACCTTATGCGATGTTTGACGAGAACATCATCGCGCAAGGAGAC	362
Db	336	GAGAAAGCGGATTCCTCCCTTAGAGATGTTTGACGAGAACGTCGTCGCTCCGAGGAGAC	395
Qy	363	GTTCCTATTGCACTTGTGCTCTCCGACGACCAAGCCCTGTAATTTCTATTGAGCT	422
Db	396	ATTAGCTATCGGACCTTGGCAATGGCCCAACGACCCGAGGCTGTGTTGCTATTGAGCT	455
Qy	423	CAACTTCATCAAGGCGGACTCATCTCACTGTCAACGGACAGACGCTGCTATGGATAT	482
Db	456	CAACTTCATTAAGGCGGACTCATCTCACTGTCAACGGACAACTGCTGCTATGGACAT	515
Qy	483	GGTAGGCAAGATGCGGTGATCGCTCTACTCTCAAGGGGTGCGGTAAAGCCATTCAC	542
Db	516	GACAGCAAGATGCAATTAATTCGCTCTCTCCTCAAGGGGTGCGGCAACGAAATCATTCAC	575
Qy	543	CGAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTGAAGA	602
Db	576	CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGACGATAGTTCTTCTCTTGAAGA	635
Qy	603	CTATACGATTGGCCCGGAGTAGATCATCAGATTTGTCAAGCTGTATGATGCTGGTGA	662
Db	636	CTACAAAGTTGGTCTGAGCTAGACCCAGATCGCAAAACC--TGGCGCTGCTGGCGA	692
Qy	663	CGCTGTTCTACGCGGTCAGTGAAGCTGGGGTCTTTCATCATTCAGGCCCAAGGCCAT	722
Db	693	CGCTCCACCGCACCGGCCAAGCAAGCTGGGGCTTCTTTTCAATTCATCTCCCAAGGCCCT	752
Qy	723	GTTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTCAGCGATCAACAAAGTTGCTGTGAC	782
Db	753	CTCGGAGCTGAAAGACGCGACCAAAAGACTCTTTGACGCGTCTGTCAGTTGTGTGCAAC	812

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DB 813 TGATGATGCTCTTTGCGCGTTTCATCTGGAATCAAACCTCGGCGTGGCTCTCGAAGAT 872  
QY 843 CGATGCTCTGACCTACCGAGTTCTGCGGTCTGTTGATGCTCGACCGGCAATGGGTGT 902  
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QY 903 CTCGACAACTACCGAGGCTCTCTCAAAACATGACTTACCAACCTCGACCAATCGGCGA 962  
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QY 963 AATCGCAACAGCTCACTCGGCGCAACAGCATCACGCTCTGTTCAAGAACTCGACCCCGC 1022  
DB 993 AATCGCAACAGCTCTGCGCAACAGCATCACGCTCTGTTCAAGAACTCGACCGTCAAGTGA 1052  
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DB 1053 TCGTTTGGCGAGAGCAACAAGCTTTGGCGAGCTACATGCTGATGGCTGCGCTGCAAGTC 1112  
QY 1083 CAACTGATCCCTGACGCTGATCGGAGCCATCTACAGGCTCATGCTGAGTTCTTGGGC 1142  
DB 1113 GAGCGCTCTCCCTGACCGCGGATCGGAATCGTCAAGCAGCATCATGCTGAGTTCTTGGGC 1172  
QY 1143 CAAAGTGGGACTCTGGGATTAAGCTTTGGGCTCGGACTGGGTAAGCCGAGACTGTGAG 1202  
DB 1173 CAAAGTGGGATGCTGGGAGTATGACTTTGGGTTGAGCTGGGTAAGCTGTGAG 1232  
QY 1203 ACGGCAATCTTTGAGCCTGTTGAGAGCTTGATGATCTTTATGCTCCCAAGAGCTGATGG 1262  
DB 1233 AAGACCTCGCTTTGAACCTTTTGGAGAGTTGATGATCTTTATGCTCCCAAGAGCTGATGG 1292  
QY 1263 CGAGTTCTGTGGCGCTTTCTCTGAGGATGAGGATATGAGCCGATTCAAGCGGATAA 1322  
DB 1293 GGAGTTACGGCTGCTCATTTCTTGAGGATGAGGATATGAGAGACTAAGCGGATGA 1352  
QY 1323 GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356  
DB 1353 GGAGTGGACCAAGTACGCAAGATATATTTGGGTAG 1386

## RESULT 4

US-10-614-954-1  
; Sequence 1, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1403  
; TYPE: DNA  
; ORGANISM: Fusarium sporotrichioides

US-10-614-954-1

Query Match 67.5%; Score 915.6; DB 16; Length 1403;  
Best Local Similarity 80.3%; Pred. No. 2.6e-306;  
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;  
QY 3 GGCCTTCAGATACAGCTCGACACCTCGGCGAGCTACCGAGGCTCTTTCGATCTACAC 62

DB 36 GTCTTTGACATAGAGCTCGACATCATCGGCAGCAACCGCTCTTCTTTCAATCTACAC 95  
QY 63 CCNAATCAGTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTTGTCAGCAC 122  
DB 96 CCAGATCAGTCTCTGTTTACCCGCTCTCTGATCCCTCCCACTATCCCACTATTCGTCAGCAC 155  
QY 123 CTTTCGAGCAAGGTCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGTGGCGAGGCCAGGTCAA 182  
DB 156 CTTTGAGGAAGGCTTAAACGCTCTCTCAACCTTCCCATGGTTCGCGGCCAGGTCAA 215  
QY 183 AGCCGAGGCAATTTAGCGAGGGAACAACAGGAATCTCTTTTATCGTCCCTTTTGGAGGACGT 242  
DB 216 GACCGAGGCAATCAGCGAAGGAACAACAGGAATCTTCCAAGATCATTTCCATATGAGGAGAC 275  
QY 243 TCCTCGTGTGTAGTGAAGAGACTTCGCGCATGATCTTTCAGCGCCCACTATCGAGGCTAT 302  
DB 276 ACCCGCTCTTGTGGTGAAGAGCTTCGCTGATGATTTCTCAGCGCCCAACGATCGAGGGGT 335  
QY 303 GAGAAAGCGGATACCTTATGCGGATGTTTGAACGAGAACATCATCGCGCAAGGAAGAC 362  
DB 336 GAGAAAGCGGCTTTCCCTTAGAGATGTTTGAACGAGAACGTCGTCGCTCCGAGGAAGAC 395  
QY 363 GTTACCTATTGACCTGTGTAATCTTCCGACGACCCAAAGCCTGTAAATCTTATTCAGCT 422  
DB 396 ATTAGCTATCGGACCTTGGCAATGGCCCAACGACCGAAGCCTGTGTTGCTATTCAGCT 455  
QY 423 CAACTTCATCAAGGCGGACTCATCTCACTCTCAACGAGACGACGCTGCTATGATAT 482  
DB 456 CAACTTCATTAAGGCGGACTCATCTCACTCAACGAGACCAATGCTGCTATGAGCAT 515  
QY 483 GGTAGGCCAAGATCGGCTGATCCGCTACTCTCCAAGGCGTCCGTAACGACCCATTCAC 542  
DB 516 GACAGGACAGATGCAATTTATTCGTTCTCTCCAAGGCGTCCGCAACGAAATCAATTCAC 575  
QY 543 CGAAGAGGAATGACCGGCAATGAACTCGATCGAAGACGATAGTTCTTTA CTTTGAATA 602  
DB 576 CGAGGAGGAATCTCGGCAATGAACTCGATCGAAGACGCTAGTCCCTCTCTCTTGAATA 635  
QY 603 CTATCAGTTGGCCCGAGGTAGATCATCAGATTTGTTCAAGCTGATGATGCTGCTGCA 662  
DB 636 CTACAAGTTGTTCTGAGCTAGACCAACAGATCGCAAAACC---TGCGCTGCTGCGCA 692  
QY 663 CGCTGTTCTCACCGCGTCAAGCTGAGTGGCGTTCTTTCATTCAGCCCCCAAGGCCAT 722  
DB 693 CGCTCCACCGCACCGGCCAAGCTGCGGCTTCTTTTTCATTCACCTCCCAAGGCCCT 752  
QY 723 GTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCAATCAACAAAGTTGCTGTCAG 782  
DB 753 CTCGAGGCTGAAGACGCGACCAAAAGACTCTTGACGCGCTGTTCCAAGTTTGTGTCAAC 812  
QY 783 TGACGATGCTCTTTTCGCGGTTTCATCTGGAATCGGCTCTCGCGTGGCTCTCGAAAGAT 842  
DB 813 TGATGATGCTCTTTTCGCGGTTTATCTGGCAATCAACCTCGCGGTACGTCGCAAGATT 872  
QY 843 CGATGGCTCTGCACCTACCGAGTTCTCGCGTCTGTTGATGCTCGACCGGCAATGGGTGT 902  
DB 873 GGATGCTTCCACACTACTGTAATCTGCGCGCTGTGACATGTCGCGGGCCCAATGGCGCT 932  
QY 903 CTCGAACAACCTACCGGCTTCTTCAAAACATGACTTACCAACCTCGACCATCGGCGA 962  
DB 933 ATCAAGCACAATACCGAGGCTCTTCAAAACATGACTTACCAACCTCGACCGTCCCGA 992  
QY 963 AATCGCAACAGTCACTCGGCGCAACAGCATCACGCTCTGTTCAAGAACTCGACCCCGC 1022  
DB 993 AATCGCAACAGTCACTTGGCGCAACAGCATCAAGCTGCTCGGACTCAACAGTGA 1052  
QY 1023 GAGCATGCGCCAGCAACAAGAGTCTCGGAGCTACTCGGACAAACACCCCGCAAGTC 1082  
DB 1053 TCGTTTGGCGAGCAACAACAGCTTTTGGCGAGTACATGCTATGCTGCTGCAAGTC 1112  
QY 1083 CAACTGATCCCTGAGGCTGATGCGGACCACTTACAGCGCTCATGCTGAGTTCTTGGGC 1142

Db	1113	GAGGCTCTCCCTGACCCCGATCGGAATCCGTCAAGCAGCATCATGCTGAGTTCCTGCGC	1172
Qy	1143	CAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGTAAGCCCGAGACTGTGAG	1202
Db	1173	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGTAAGCCTGAGAGTGTGAG	1232
Qy	1203	ACGCCAATCTTTGAGGCTGTCAGAGCTTGATGATGATTTATGCCCAAGAGCCTGATGG	1262
Db	1233	AAGACCTCGCTTTGAACCTTTGAGAGTTTGTATGATGATTTATGCCCAAGAGCCTGATGG	1292
Qy	1263	CGAGTTCGTGCGGCGCTTCTCTGAGGATGAGGATATGAGCCGATTGAGGCGGATGA	1322
Db	1293	GGAGTTTACGCGCTCCMTTCTCTGAGGATGAGGATATGAGAGACTAAGGCGGATGA	1352
Qy	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	1353	GGAGTGGACAAAGTACGCAAGTATATTTGGTAG	1386
RESULT 5			
US-10-074-279-11			
; Sequence 11, Application US/10074279			
; Publication No. US20020162136A1			
; GENERAL INFORMATION:			
; APPLICANT: Hohn, T.			
; APPLICANT: Salmeron, J.			
; APPLICANT: Peters, C.			
; APPLICANT: Kendra, D.			
; APPLICANT: Reinders, J.			
; APPLICANT: Kuznia, R.			
; APPLICANT: Dill-Mackey, R.			
; TITLE OF INVENTION: Transgenic Plant and Methods			
; FILE REFERENCE: sequence list			
; CURRENT APPLICATION NUMBER: US/10/074,279			
; CURRENT FILING DATE: 2002-02-12			
; PRIOR APPLICATION NUMBER: US/09/538,414			
; PRIOR FILING DATE: 2000-03-29			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 11			
; LENGTH: 12949			
; TYPE: DNA			
; ORGANISM: Plasmid			
US-10-074-279-11			
Query Match			
Best Local Similarity 67.5%; Score 915.6; DB 13; Length 12949;			
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
Qy	3	GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACCAGGCTCTCTTTGATCTACAC	62
Db	11281	GTCTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTCTTTCAATCTACAC	11340
Qy	63	CCMAATCAGTCTCTCTACCCGCTCTGATTCCTCTCAATATCCCACTATTGTGAGCAC	122
Db	11341	CCAGATCAGTCTCGTTTACCCGCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC	11400
Qy	123	CTTTCGAGCAAGGTCTTAAGCGCTTCGCCAAGCCGTCCTATGGTCCGAGCCAGGCTCAA	182
Db	11401	CCTTGAGGAAGGCTTAAGCGCTCTCTCAACCTTCCCATGGTCCGCGGCCAGGTCAA	11460
Qy	183	AGCCGAGGCAATTAGCGAGGAACAACAGGAATCTCTCTTTATCGTCCCTTTTGAGGACGT	242
Db	11461	GACCGAGGCAATCAGCGAAGGAACAACAGGAATCTCTCAAGATCATTTCCATATGAGGAGAC	11520
Qy	243	TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTCTGAGGCGCCCAACATCGAGGGTAT	302
Db	11521	ACCCCGTCTGTGTGAAGACCTCGGTGATGATCTCTGAGGCGCCCAACATCGAGGGT	11580
Qy	303	GAGAAAGCGGGATACCTCTATGCGATGTTGACGAGACATCATCGCCCAAGGAGAC	362
Db	11581	GAGAAAGCGGGTTCCTCTTAGATGATGTTGACGAGAACGTCGTCGCTCCGAGGAAGAC	11640

RESULT 6  
US-10-614-954-11  
; Sequence 11, Application US/10614954  
; Publication No. US20040034884A1

Qy	363	GTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCCTGTAAATCTATTGACGCT	422
Db	11641	ATTAGCTATCGGACCTGGCAATGGCCCAACGAGCCCGCTGTGTGCTATTGACGCT	11700
Qy	423	CAACTTCATCAGGGCGGACTCATCTCCTCACTGTCAACGGACGACGCGTCTATGGATAT	482
Db	11701	CAACTTCATTAAGGGCGGACTCATCTCACCGTCAACGGCAACATGGTGTCTATGGACAT	11760
Qy	483	GSTAGGCCAAGATGCGGCTGATCCGTCTACTCTCAAGGGGTGCGTAACAGACCATTCAC	542
Db	11761	GRACAGACGAAGTGCATTAATTTGCTCTCTCAAGGGGTGCGCAACGAATCATTCAC	11820
Qy	543	CGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGAGATAGTTCCTTCACTTGAATA	602
Db	11821	CGAGGAGAAATCTCGGCCATGAACCTCGATCGCAAGAGATAGTTCCTTCACTTGAATA	11880
Qy	603	CTATACGATTTGGCCCGAGGTAGATCATCAGATTGTCAAGCTGATGTAGTCTGGTGTGA	662
Db	11881	CTACAAAGTTGGTCTGAGCTAGACCACGAGATCGCCAAACC--TGCGCTCTCTGGCGA	11937
Qy	663	CGCTGTTCTCACGCCGCTCAGTGCAGCTGGGGCTTCTTCAATTCAGCCCCCAAGGCCAT	722
Db	11938	CGCTCCACCGGCACCGGCCAAGGCAAGCTGGGGCTTCTTTCATTCATCTCCCAAGGCCCT	11997
Qy	723	GTGAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGATCAACAAAGTTCGTGTGAC	782
Db	11998	CTCGAGCTGAAAGACGCGACCAAAAGACTCTTGACGGCTCGTCCAAGTTTGTGTCAAC	12057
Qy	783	TGACGATGCTCTTTGGCGTTTCATCTGGAATCGGCTCTCGCGTGGTCTCGAAAGAT	842
Db	12058	TGATGATGCTCTTTGGCGTTTATCTGGCAATCAACCTCGCGCTAGTCTTCGCAAGAT	12117
Qy	843	CGATGCTCTGCACTTACCGAGTTCTGCGTGTCTGTGATGCTCGACCGGCAATGGTGT	902
Db	12118	GSATGCTTCCACACTTACTGAATTCGCGCGCTGTGACATCGGGGGCCCAATGGCGT	12177
Qy	903	CTCGAAACTACCCAGGCTTCTTCAAAACATGACTTACCACAACTCGACCAATCGGCGA	962
Db	12178	ATCAAGCATATACCCAGGCTTCTTCAAAACATGACTTACCACAACTCGACCGTCCGCA	12237
Qy	963	AATCGCCACGAGTCACTCGGCGCAACAGCATCAAGCTTCTGTTGAGAACTCGACCCGCG	1022
Db	12238	AATCGCCACGAAACCACTTTGGCGCAACAGCATCAAGCTTCTGTTGAGAACTCGACCGT	12297
Qy	1023	GAGCATGCGCCACGAAACAGAGGCTCTCGCGAGTACCTGCAACAAACCCGACAAATC	1082
Db	12298	TGCTTTGCGCACGACGAAACAGAGCTTTGCGGAGTACATGCTGCTGCTGACAGTCT	12357
Qy	1083	CAAGCTATCCCTGACGGCTGATGCGGACCCATCTTACCAGCTCATGCTGAGTTCCTGGG	1142
Db	12358	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAGCAGCATCATCTGAGTTCCTGGG	12417
Qy	1143	CAAGTGGGACTCTGGGATACGATTTGGGCTCGGACTGGGTGAGTAAAGCCGAGACTGTAG	1202
Db	12418	CAAGTGGGATGCTGGGATGATGACTTTGGGTTTGGACTGGGTGAGTAAAGCCGAGTGTAG	12477
Qy	1203	ACGGCCAAATCTTTGAGCGCTGTTGAGAGCTTGTGATCTTTATGCCCAAGAGCTCATGG	1562
Db	12478	AGACCTCGCTTTGAACCTTTTGAAGTTTGAATGATCTTTATGCCCAAGAGCTCATGG	12537
Qy	1263	CGAGTTCGTGCGGCTTCTCTGAGGATGAGGATATGAGCCGATTAAGAGCGGATAA	1322
Db	12538	GGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATATGAGGATTAAGAGCGGATTA	12597
Qy	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	12598	GGAGTGGACCAAGTATGCGCAGTATATTTGGGTAG	12631

```

; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
; US-10-614-954-11

Query Match          67.5%; Score 915.6; DB 16; Length 12949;
Best Local Similarity 80.3%; Pred. No. 8.1e-306;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY      3  GGTCTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAGGCTCTCTTTGATCTACAC 62
DB      11281  GTCTTTTGACATAGAGCTGCATCATCGGCCAGAACCGCTCTCTTTCAATCTACAC 11340

QY      63  CCAATFAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCATTTATGTCAGCAC 122
DB      11341  CCAGATCAGTCTGTTTACCCGCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 11400

QY      123  CTTTCGAGCAAGGCTTTAAGGCTTCTCCGAGCGTCCCATGGTCCGACGGCCAGGTCAA 182
DB      11401  CTTTGAGGAAGGCTTAAAGCGCTCTCTCAAACTTTCCCATGGTCCGCGGCCAGGTCAA 11460

QY      183  AGCCGAGGCAATPAGCGAGGGAACACAGAACTCTCTTATCGTCCCTTTTGAGGACGT 242
DB      11461  GACCGAGGCAATCAGCGAAGGAACACAGAACTCTCAAGATCATTTCCATATGAGGAGAC 11520

QY      243  TCCCTGTTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCCAACGATCGAGGGTAT 302
DB      11521  ACCCGCTCTTGTGTGAAGACCTCCGCGATGATTCCTCAGCGCCCAACGATCGAGGGT 11580

QY      303  GAGAAAGCGGGATACCTCTATGCGATGTTGACGAGAACATCATCGCGCCAGGAGAC 362
DB      11581  GAGAAAGCGGGTTTCCCTCTAGAGATGTTGACGAGAACGTCGTCGCTCCGAGGAAGAC 11640

QY      363  GTTACCTATTGGACCTGGTACTCGTCCGACGACCCAAAGCCCTGTAAATCTATTGCACT 422
DB      11641  ATTAGTATCGGACCTTGGCAGTATGGCCCAACGACCGGAGCCCTGTGCTATTGCACT 11700

QY      423  CAACTTCATCAAGGCGGACTCATCTCTCACTGTCAAACGACGACACGGTGTCTATGATAT 482
DB      11701  CAACTTCATTAAGGCGGACTCATCTCTCACTGTCAAACGACGACACGGTGTCTATGACAT 11760

QY      483  GGTAGCCCAAGATGCGGTGATCGGTCTACTCTCAAGGGTCCGCTAAACGCCATTTCAC 542
DB      11761  GACAGGCAAGATGCAATTAATTCGTCTCTCTCAAGGGTCCGCTAAACGCCATTTCAC 11820

QY      543  CGAAGAGGAATCAGCGCCATGAACCTCGATCCCAAGACGATAGTTCCTTACCTCAAAA 602
DB      11821  CGAGGAGGAATCTCGGCCATGAACCTCGATCCCAAGACGATAGTTCCTTCAAAA 11880

QY      603  CTATACGATTGGCCCGAGGTAGATCATTCAGATGTCAAAGCTGATGTAGCTGGTGTGA 662
DB      11881  CTACAAGTGGTCTGAGCTAGACACCAACAGATCGCCAAACC---TGGCGCTCTGCGCA 11937

QY      663  CGCTGTTCTCAGCGCGTCTAGTCCAGCTGGCGTCTTCAATTCAGCTCAGCCCAAGCCAT 722
DB      11938  CGCTCCACCCGCAACCGCCCAAGGCAAGCTGGCGTCTTCTTTCAATTCATCTCCCAAGGCCCT 11997
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QY      723  GTCAGAGCTCAAGGATGCTGTCTACCAAGATCTTTGACGATCAACAAGTTGCTGTGAC 782
DB      11998  CTCGGAGCTGAAAGACGACGAGCCACAAAGACTCTTGACGCTGCTCAAGATTGCTCAAC 12057

QY      783  TGACATGCTCTTTTCGGGCTTCATCTGGAATCGGCTCTCGCGTCCGCTCTCGAAGAT 842
DB      12058  TGATGATGCTCTTTTCGGGCTTTATCTGCAATCAACCTCGCGCTACGCTCTCGAAGAT 12117

QY      843  CGATGCTCTGCACCTACCGAGTTCTCGCGTCTCTGTATGCTCGACCGGCAATGGGTGT 902
DB      12118  GGATGCTTCCACACTACTGAAATCTCGCGCTCTGACATGCGGGGCCCAATGGGCT 12177

QY      903  CTCGAACAACCTACCCAGGCTCTTTCAAACAATGACCTTACCAAACTCGAATCGGGA 962
DB      12178  ATCAAGCACATACCCAGGCTCTTTCAAACAATGACCTTACCAAACTCGAATCGGGA 12237

QY      963  AATGCCAACAGTCACTCGGGCGAACAGCATCAAGCTTGGTTCAGAACTCGACCCGCG 1022
DB      12238  AATGCCAACAGCAACCTTGGCGCAACAGCATCAAGCTTGGCTCGGAACCTCAACAGTGA 12297

QY      1023  GAGCATGCGCCAGCAACAAGAGGTCTCGCGAGCTACCTGCAACAACCCCGCAAGTTC 1082
DB      12298  TCGTTTGGCAGACGAAACAAGCTTTGGCGAGCTACATGATGCTGCTGACAGTTC 12357

QY      1083  CAACTGATCTCTGACGGCTGATGCGGACCCATCTACCAAGGCTCATGCTGAGTCTTGGGC 1142
DB      12358  GAGCGTCTCTCTGACGGCTGATGCGGATCGAATCCGCTCAAGCAGCATCATGCTGAGTCTCTGGGC 12417

QY      1143  CAAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGGGTAAAGCCGAGAGCTGTAG 1202
DB      12418  CAAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCCTGAGAGTGTAG 12477

QY      1203  ACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTAATTTATGCCCAAGAGCCCTGATGG 1262
DB      12478  AAGACTCGCTTTGAACCTTTGAGAGTTTGTATGTAATTTATGCCCAAGAGCCCTGATGG 12537

QY      1263  CGAGTTCGTGCGGCGCTTCTCTGAGGATGAGGATATGGAACCGATTGAAGGCGGATAA 1322
DB      12538  CGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATATGGAAGACTAAAGCGGATGA 12597

QY      1323  CGAGTGGAACAGTATGCGAGTACGTTGGTTAG 1356
DB      12598  CGAGTGGAACAGTATGCGAAAGTATATTGGGTAG 12631
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## RESULT 7

US-10-074-279-10

; Sequence 10, Application US/10074279

; Publication No. US20020162136A1

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequencelist

; CURRENT APPLICATION NUMBER: US/10/074,279

; PRIOR FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: US/09/538,414

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 13737

; TYPE: DNA

; ORGANISM: Plasmid

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Plasmid

US-10-074-279-10

Query Match		67.5%;	Score 915.6;	DB 13;	Length 13737;
Best Local Similarity		80.3%;	Pred. No. 8.4e-306;		
Matches 1087;		Conservative	0;	Mismatches 264;	Indels 3; Gaps 1;
Qy	3	GGCTTTCAAGATACAGCTCGACACCTCGCGCAGCTTACAGGCTTCCCTTTCGATCTACAC	62		
Db	50	GTCTTTTGATAGAGCTCGACATATCGCGCAGCAACCGCTCTCTTTTCAATCTACAC	109		
Qy	63	CCAAATCAGTCTCTTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTGTCAGAC	122		
Db	110	CCAGATCAGTCTGTTTACCCGCTCTCTGATCCCTCCAGTATCCACCATGTCAGAC	169		
Qy	123	CTTCGAGCAAGGCTTTAAGCGTTCTCGAAGCGCTCCATGGGTGCGAGGCCAGGTCAA	182		
Db	170	CCTTGAGGAAGGCTTAAACCGCTCTCTCAAACCTTCCCATGGGTGCGCGGCGAGGTCAA	229		
Qy	183	AGCCGAGGCGATAGGAGGGAACACAGAACTCTCTTATCGTCCCTTTTGAGGAGCT	242		
Db	230	GACCGAGGCGATCAGCGAAGGAACACAGAACTTCCAAAGATCATTTCCATATGAGGAGAC	289		
Qy	243	TCCTCGTGTGTAGTAAAGACCTCGCGATGATCTTTCAGGCGCCACCATCGAGGGTAT	302		
Db	290	ACCCGCTCTTGTGTGAAGACCTCGGTGATGATCTCTCAGCGCCCAACCATCGAGGGGTT	349		
Qy	303	GAGAAAGCGGATACCTTATGGCGATGTTTGAOGAGAACATCATCGCGCCCAAGGAAGAC	362		
Db	350	GAGAAAGCGGTTTCCCTTAGAGATGTTTGAOGAGAACGTCGTGCTCCGAGGAAGAC	409		
Qy	363	GTATCCTATTGACCTGTGTACTGTCCTCCGACGACCCAAAGCCCTGTAAATCTATTGCGCT	422		
Db	410	ATTAGCTATCGGACCTGGCAATGGCCCCAACGACCCGAAAGCCGTGTGCTATTGCGCT	469		
Qy	423	CAACTTCATCAAGGGCGGACTCATCTCTCACTGTCAACGACAGCAGCGTGTATGATAT	482		
Db	470	CAACTTCATTAAGGGCGGACTCATCTCACTGTCAACGACAGCAGCAGTGTATGAGCAT	529		
Qy	483	GGTAGGCCAAGATGCGGTGATCGCTACTCTCTCAAGGGCGTCCGTAACGACCCCAATTCAC	542		
Db	530	GACAGGACAAGATGCAATTAATTCGTCTCTCTCAAGGGCGTCCGCAACGAATCATTCAC	589		
Qy	543	CGAAGGGAATGACGGCCATGACCTCGATCGCAAGACGATAGTTCCTTACCTTGAATAA	602		
Db	590	CGAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGCGGTAGTCCCTCTCTTGAATAA	649		
Qy	603	CTATACGATTGCCCGAGGTAGATCATCAGATTGTCAAAGCTGTAGTGTGTGTGCA	662		
Db	650	CTACAAGTTGGTCTGAGCTAGACCAACAGATCGCAACCC---TGCCTGTGTGGCGA	706		
Qy	663	CGCTGTTCTCAGCGGTCAGTGCAAGCTGGGCGTTCTTTCATTCAGGCCCAAGGCCAT	722		
Db	707	CGCTCCACCGCAGCGGCCAAGCAAGCTGGGCGTTCTTTCATTCACCTCCCAAGGCCCT	766		
Qy	723	GTGAGAGCTCAAGATGCTGTACCAAGACTCTTGAAGCATCAACAAAGTTCGTGTGAC	782		
Db	767	CTCGAGCTGAAAGACGACGCCACAAAGACTCTTGACGGCTGCTCAGAGTTGTGTCAAC	826		
Qy	783	TCAGCATGCTCTTTGGCGTTTCATCTGGAATCGGCTCTCGCGTGGCTCTCGAAGAT	842		
Db	827	TGATGATGCTCTTTGGCGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGAAGAT	886		
Qy	843	CGATGCTCTGCACTTACCGAGTTCTGCGGTGCTGTGTGATGTGCAACCGGCAATGGGT	902		
Db	887	GGATGCTTCCACACCTACTGMAATCTGCGCGCTGTGCGATCGCGGGGCCAATGGCGT	946		
Qy	903	CTCGAACAATACCCAGGCTTCTTCAAACATGACCTACCAACTCGACCATCGGCGA	962		
Db	947	ATCAAGCATATACCCAGGCTTCTTCAAACATGACCTACCATGACTCGACCGCTCGCCGA	1006		
Qy	963	ATCGCCACGAGTCACTCGGCGCAACAGCATCAGCCCTTCTGTTAGAACTCGACCCCGC	1022		
Db	1007	AATCGCCCAAGAACCACTTTGGGCGCAACAGCATCAGCCCTGCGCTCGGAATCAACAGTGA	1066		

Qy	1023	GAGCATGCGCCAGCGAAACAGAGGTTCTCGGAGGTACCTGACACAAACCCCGACAAGTC	1082
Db	1067	TCGTTTGGCAGACAGAAAGCTTTGGCGAGCTATACATGCGCTCGCTGACAAGTC	1126
Qy	1083	CAACGTATCCCTGACGGCTGATGCGGACCCATCTACACGCGTCATGCTGAGTCTTTGGGC	1142
Db	1127	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTCTTGGGC	1186
Qy	1143	CAAGTGGGACTCTCGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTGAG	1202
Db	1187	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCTGAGAGTGTGAG	1246
Qy	1203	ACGGCCAATCTTTGAGCCCTGTTGAGAGCTTGATGACTTTATGCCCAAGACCTGATGG	1262
Db	1247	AAGACCTCGCTTTGAACCTTTTGAAGTTTGAATTTATGCTTATGCCCAAGACCTGATGG	1306
Qy	1263	CGAGTCTGTGCGGCGCTTCTCTGAGGATGAGATATGGACCGATTCAAGGCGGATAA	1322
Db	1307	GGAGTTACGGGCTCATTTTCTGAGGATGAGGATATGGAGACTTAAAGGCGGATGA	1366
Qy	1323	GGAGTGGACCAAGTATGCGCAGTACGTTTGGTTAG	1356
Db	1367	GGAGTGGACAAAGTACGCAAGTATATTGGGTAG	1400

RESULT 8  
US-10-614-954-10  
; Sequence 10, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 13737  
; TYPE: DNA  
; ORGANISM: Plasmid  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
US-10-614-954-10

Query Match		67.5%;	Score 915.6;	DB 16;	Length 13737;
Best Local Similarity		80.3%;	Pred. No. 8.4e-306;		
Matches 1087;		Conservative	0;	Mismatches 264;	Indels 3; Gaps 1;
Qy	3	GGCTTTCAAGATACAGCTCGACACCTCGCGCAGCTTACAGGCTTCCCTTTCGATCTACAC	62		
Db	50	GTCTTTTGATAGAGCTCGACATATCGCGCAGCAACCGCTCTCTTTTCAATCTACAC	109		
Qy	63	CCAAATCAGTCTCTTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTGTCAGAC	122		
Db	110	CCAGATCAGTCTCTTTTACCCGCTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC	169		
Qy	123	CTTCGAGCAAGTCTTAAAGCGCTTCTCCGAGCGCTCCCATGGGTGCGAGGCCAGGTCAA	182		
Db	170	CCTTGAGGAAGGCTTAAACCGCTCTCTCAAACCTTCCCATGGGTGCGGCGCAGGTCAA	229		
Qy	183	AGCCGAGGCGCATTTAGCGGGAACACAGAACTCTCTTTTATCGTCCCTTTTGAGGACGT	242		
Db	230	GACCGAGGCGCATCAGCGAAGGAACACAGAACTTCCAAAGTCAATTCATATGAGGAGAC	289		



243 TCCTCGTGTGTAGTAAGACCTCGCGATGATCTTTCAGCGCCACGATCGAGGTAT 302  
Db |||||  
290 ACCCGCTCTTGTGTGAAGACCTCGTGATGATCTTTCAGCGCCACGATCGAGGTAT 349  
Qy |||||  
303 GAGAAAGCGGGATACCTATCGCGATGTTTGAAGAAACATCATCGCGCCAGGAAGAC 362  
Db |||||  
350 GAGAAAGCGGGTTCCTTGAAGATGTTTGAAGAAACGTCGTCTCCGAGGAAGAC 409  
Qy |||||  
363 GTTACTATTGACCTGTGCTGCTCCGACGACCAAGACCTGTAAATTTCTATTGCGCT 422  
Db |||||  
410 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCGGAAGCTGTGTGCTATTGCGCT 469  
Qy |||||  
423 CAACTTTATCAAGGGCGGACTCATCTCACTGTCAACGACGACGCGGTGCTATGATAT 482  
Db |||||  
470 CAACTTTATTAAGGGCGGACTCATCTCACTGTCAACGACGACGCGGTGCTATGATAT 529  
Qy |||||  
483 GGTAGCCCAAGATGCGGTGATCGGTCTACTCTCAAGGGCGGTGCGTAAGACCCATTAC 542  
Db |||||  
530 GACAGGACAAGATGCAATTTATTCGTCTCTCAAGGGCGGTGCGTAAGACCCATTAC 589  
Qy |||||  
543 CGAAGAGGAATGACGGCCATGAACCTCGATCGAAGACGATAGTTTCTTACCTTGAAAA 602  
Db |||||  
590 CGAGGAGGAATGCTCGGCCATGAACCTCGATCGAAGACGATAGTTTCTTCTTGAANA 649  
Qy |||||  
603 CTATAGCATTTGCGCGGAGTATCATCAGATTGTCAAAGCTGATGTAGCTGGTGTGA 662  
Db |||||  
650 CTACAAAGTTGCTCTGAGCTAGACCAACAGATCGCAAAAC---TGCGCTGCTGGCGA 706  
Qy |||||  
663 CGCTGTTCTACGCGGTCAGTGCAAGCTGGGGTCTTCAATTCAGGCCCAAGCCAT 722  
Db |||||  
707 CGCTCCACCGCACCGGCCAAGCAAGCTGGGGTCTTCAATTCAGGCCCAAGCCAT 766  
Qy |||||  
723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTGACGATCAACAAAGCTGCTGTGCGAC 782  
Db |||||  
767 CTCGGAGCTGAAGACGACGACCAAGACTCTTGACGCTGCTCCAAGTTTGTGTCAAC 826  
Qy |||||  
783 TGAAGATGCTTTTTCGGGCTTCATCTGGAATTCGGCTCTCGCGTGTGCTCGAAGAAAT 842  
Db |||||  
827 TGATGATGCTTTTTCGGGCTTCATCTGGAATTCGGCTCTCGCGTGTGCTCGAAGAAAT 886  
Qy |||||  
843 CGATGCTCTGACCTTACGAGTCTCGCGTGTGCTGATGCTCGACCGGCAATGGGCT 902  
Db |||||  
887 GGAATGCTTCCACACTTACTGAAATTCGCGCGCTGTCGACATGCGGGGCCCCAATGGGCT 946  
Qy |||||  
903 CTCGAACAACTACCAAGGCTCTTCAAAACATGACCTACCAAACTCGACCATCGGCGA 962  
Db |||||  
947 ATCAAGCATATCCAGGCTCTTCAAAACATGACCTACCAAACTCGACCATCGGCGA 1006  
Qy |||||  
963 AATCGCAACAGATCTCTCGGCGCAACAGCATCACGCTTGTGTAAGAACTCGACCCCGC 1022  
Db |||||  
1007 AATCGCAACAGATCTCTCGGCGCAACAGCATCACGCTTGTGTAAGAACTCGACCCCGC 1066  
Qy |||||  
1023 GAGCATGCGCCAGCAAGAGGCTCTCGAGCTACCTGCAACAAACCCGACAAAGTC 1082  
Db |||||  
1067 TCGTTTTCGCGAGCAAGACCTTTGGCGAGTACATGATGCGCTGCTGCAAGATC 1126  
Qy |||||  
1083 CAACTGATCTCCTGACGCTGATCGGACCCATCTACAGCGTCAATGCTGATTTTGGGC 1142  
Db |||||  
1127 GAGCGTCTCCCTGACGCGCGATCGAATCGTCAAGCAGCATCATGCTGATTTCTGGGC 1186  
Qy |||||  
1143 CAAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGGACTGGGTAAGCCGAGCTGTAG 1202  
Db |||||  
1187 CAAAGTGGGATGCTGGGATTAAGACTTTGGGCTGGGCTGGGTAAGCCGAGCTGTAG 1246  
Qy |||||  
1203 ACGGCCAATCTTTGAGCTGTCAGAGCTTGTATCTTATCCCAAGAGGCTCATGG 1262  
Db |||||  
1247 AAGACCTCGCTTTGAACTTTGAGAGTTGATGATCTTTATGCCCAAGAGGCTGTAG 1306  
Qy |||||  
1263 CGAGTTCTGTGCGCGCTTTCTCTGAGGATGAGGATATGGAACCGATTTGAAGCCGATAA 1322  
Db |||||  
1307 GGAATTTACGCGCTCCATTTCTCTGAGGATGAGGATATGGAAGCTAAAGCCGATGA 1366  
Qy |||||  
1323 GGAGTGCAACAGATGCGCAGTACGTTGGTTAG 1356

Db |||||  
1367 GGAGTGCAACAGTACGCAAGATATATTGGGTAG 1400

RESULT 9  
US-10-074-279-7  
; Sequence 7, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1425  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-10-074-279-7

Query Match 18.4%; Score 249.8; DB 13; Length 1425;  
Best Local Similarity 51.9%; Pred.No. 3.6e-75;  
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

Qy 16 CAGCTCGACACCTCGCGCAGCTACAGGCTCTTTCGATCTACACCCCAATCAGTCTC 75  
Db 64 CAACTGATATTTTGGGACAAACCTTCGATACAAATATACATACATATGCTCT 123  
Qy 76 CTCTACCCCGCTCTGATTCCTCAATATCCACTATTGTGACGACCTTCAGCAAGGT 135  
Db 124 ATCTACCGGTGACACAGATCTTCTGCTATGACCATATCGTAAATACCTTAAACAAGGA 183  
Qy 136 CTTAAGCGCTTCTCGAAGCGTCCATGGTGGGAGGAGTCAAGCCAGGCGCAT 195  
Db 184 CTGAAACATTCGGCTTAAATAATTCAGTGGCTAGCAGGAATGTCGTAATGAGGTCT 243  
Qy 196 AGCGAGGGAACACAGGAACCTTCTTTATGCTCCCTTTTGGAGACGTTCTCTGTGTGA 255  
Db 244 GACGAAGGTAACTGTTACCTACAGAAATGTCCTGACAGCAAAATTCAC---TTATC 300  
Qy 256 GTGAAGACCTCGCGATGATCTCTTACGGCCCGACGATCGAGGTATGAGAAGCGGGA 315  
Db 301 GTCCAAGATCTTCGAGAAGATCTGTCTGCCCAACAATGGATTCGCTTGAANAAGCTGAC 360  
Qy 316 TACCTATGCGCATGTTTGAACGAGACATCATCGGCCCAAGGAAGACGTT-----ACCT 369  
Db 361 TTTCTATCTCATGTTTGAACGAGAAAGCTTTTGGCTTGTGATGATCATCACTCACT 420  
Qy 370 ATTGACCTGTTGTTGTTCCCGACGACCCCAAGCCCTGTAATTTCTATTGAGCTCAACTTC 429  
Db 421 GGAACACATATAGTATGGCCCGCCAGAGTGGGCTGTATTTGCACTTCAAGCAAACTTT 480  
Qy 430 ATCAAGGGCGGATCATCTCTCTCACTGTCACGACGACGAGCTGCTATGATATGGTAGGC 489  
Db 481 ATCTCGGCGGCTGCTCTTAACTATTGTCGGGACGACAAATATTATGATATAACAGGA 540  
Qy 490 CAAAGTGGCTGATCCGCTACTCTCAAGGGTGGCGTAACGACCATTCACCCGAGAG 549  
Db 541 CAGGAAGTATCATCACTTGTCTCAATAATCTTGGCAACCAAAACCTTTCTCTGATGA 600  
Qy 550 GAAATGACGGCCATGAACCTCGATCCAAAGACGATAGTTCTTTA CTTTGAAACATATACG 609  
Db 601 GAACTGCTCATTTGGAATATAGATAAAAGCAAACTATTTCTTTGTTGATGAACCTTGG 660



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QY 610 ATT---GGCCCCGAGGTAGATCATCATGATGTCACAAAGCTGATGTAGCTGGTGGTACGCT 666
Db 661 GAAACCCGACACACGCTAGTTCATGAATAGTGGAAACCTCTAGAAATCAAAAGTGGAGAG 720
QY 667 GTTCTCACCGCGGTGAGT-----GCAAGCTGGCGGTCTTTCACATTCAGCCCCAAG 717
Db 721 GAAAGGAACAGCTGTTGTTCTTCGAACTCTACTTGGGCTTATGTTGAAATTTTCTGCTATC 780
QY 718 GCATGTCAGAGCTCAAGGATGCTGCTCAACAGATCTTTGAGCATCAACAAAGTTTCGTG 777
Db 781 TCATTGCAGATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
QY 778 TGACATGACGATGCTCTTTTGGCGTTTCATCTGGAATTCGGCCCTCTCGCGTGGCTCTCGAA 837
Db 841 TCCACTGATGATATCGTCACTGCTTTTCATCTGGAATCAGATTTCTCGAGCCGTTTATCT 900
QY 838 AGAATCGATGGCTCTGACCTACCGAGTTCTCGCGTGTCTGCGTGTCTGATGCTCGACCGCAATG 897
Db 901 CGACTTAAACCGAAGCAAAATCAAAATTTAGGCGGTCTGCTGATGTTAGAAAACGGCTA 960
QY 898 GGTGTCTCGAAACAACTACCCAGGCTTCTTCAAAACATGACCTTACCACAACTCGACCATC 957
Db 961 GGACTCCCGAAACGATATCCAGGTTATTAGTCAACATGACCTTTTAATACAGTTCCCTG 1020
QY 958 GCGAAATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCGTTTCAGAACTCGAC 1017
Db 1021 AAAAGCTTGGATCATAAAAGTTTGGCGGTTCTTGCAATCAGATTCGCAAGGCTTAGAC 1080
QY 1018 CCGCGGAGCA-----TGGCGCAGCGCAACAGAGGTCTCGAGCTGCTGACACAAAC 1071
Db 1081 CTTAAAGTCTTCGATTTGGCTTATAATACATGCGCATCTTGTACGCTCTTACCGGATGC 1140
QY 1072 CCGCAAGTCCAAACGTATCCCTGACGGCTGATGCGGACCCATCTACACAGCGTCATGCTG 1131
Db 1141 CCGACACAGCTAAGTTTCTATACCTCAACCAATTTGATCTTCTGGAATTTAGTCT 1200
QY 1132 AGTTCTTGGGCAAGTGGGACTCTGGGATTAAGCACTTTGGGCTCGGACTGGGTAAAGCCC 1191
Db 1201 AGTTCTGGGCAAAAGTCAGCGCTGATGAGCTTGAATTTCAATCTAGGGCTTGGGAAGCCC 1260
QY 1192 GAGACTGTAGACGGCAATCTTTGAGCTGTGAGCTGTGAGAGCTTGATCTTTATGCCCAAG 1251
Db 1261 AAGAGTGTACGACGGCGCGCTTCATTTCCCTTGAGAGCTAATATATTTTATGCCCTAGA 1320
QY 1252 AAGCTGTATGGCGAGTCTGTGGCGGCTTCTCTGAGGAGTACGAGATATGACCGATG 1311
Db 1321 TCCTCAGAGGTGAATGTTGTTGCTCTTTGGCTTAGAGTAAGATTTGGGAGTGCCTG 1380
QY 1312 AAGGCGGATAAGGAGTGGACCAAGTATGC 1340
Db 1381 AATGCGGATAAAGATGGACAAATTTATGC 1409
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RESULT 10

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US-10-614-954-7
; Sequence 7, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-7
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Query Match 18.4%; Score 249.8; DB 16; Length 1425;
Best Local Similarity 51.9%; Pred. No. 3.6e-75;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;
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QY 16 CAGCTCGACACCTCGGCCAGCTACGAGCCCTCTTCGATCTACACCCAAATCACTCTC 75
Db 64 CAACCTTGATATTTTGGGACAAACACCTTCGCTATACAACTATACACTCAATATGCTCT 123
QY 76 CTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGAGCACTTTCGAGCAAGGT 135
Db 124 ATCTACCGGTGACAGATCTCTTCTGCTCATGACCATATGTAATACCTTTAACAAGAGA 183
QY 136 CTTAAGCGCTTCTCGAAGCGTCCCATGGTGGAGCCAGGTCAAGCCGAGGCGCAT 195
Db 184 CTTGAAACATTTGGCTTAAATAATTTCCAGTGGCTAGCAGGAAATGTCGTAATGAAGGTCT 243
QY 196 AGGAGGGAACACAGGAACTTCTTATCGTCCCTTTTGGAGACGTTCTCTGTTGTA 255
Db 244 GACGAAGGTAAACACTGGTACCTACAGAAATGTCGCTGACAGCAAAATTCAC---TTATC 300
QY 256 GTGAAGAGCTCCGCGATGATCTTTCAGCGCCACGATCGAGGATATGAAAGGCGGGA 315
Db 301 GTCCAAAGATCTTCGAGAGATCTGTCTGCCCAACANTGGATTCGTTGAAAAGCTGAC 360
QY 316 TACCTATGGCGATGTTTGAACGAGAACATCATCGCGCCAAAGGAAGACGTT-----ACCT 369
Db 361 TTTCTCTATCTACATGTTAGACGAAAAGACTTTTGGCGCTTGCATGACTATCAATCCACCT 420
QY 370 ATTGACCTGGTACTGGTCCCGACGACCAAGCCCTGTAATTTCTATGAGCTCACTTC 429
Db 421 GGAACACATATAGGTATGGCCCGCAAGTGGCGCTGTTATTTGCACTTCAAGCAAACTTT 480
QY 430 ATCAAGGGCGGACTCATCTCTCACTGTCAACGACAGCAGCGGTCTATGATATGTTAGGC 489
Db 481 ATCTCGGCGGCTGCTTAACTATTGTCGGGACGACAAATATATGATATTAACAGA 540
QY 490 CAAGATGCGGTGATCGTCTACTCTCAAGGGCGTCCGTAACGACCATTCACCGAAGAG 549
Db 541 CAGGAAAGTATCATCAACTGCTCAATAATCTTGCACCAAAAACCTTTCTGATGAA 600
QY 550 GAAATGACGGCCATGAACTCGATCGAAGACGATAGTTTCTTACCTTCCCTGAAACTATACG 609
Db 601 GAACTGCTCATTTGGAATAATATAGATAAAAGCAATCTATTCTCTTGTGATGAAACTGG 660
QY 610 ATT---GGCCCCGAGGTAGATCATCATGATTTGCAAGCTGATGTAGCTGGTGGTACGCT 666
Db 661 GAAACCCGACACACGCTAGTTCATGAATAGTGGAAACCTCTAGAAATCAACAGTGGAGAG 720
QY 667 GTTCTCACCGCGGTGAGT-----GCAAGCTGGCGGTCTTTCACATTCAGCCCCAAG 717
Db 721 GAAAGGAACAGCTGTTGTTCTTCGAACTCTACTTGGGCTTATGTTGAAATTTTCTGCTATC 780
QY 718 GCATGTCAGAGCTCAAGGATGCTGCTCAACAGATCTTTGAGCATCAACAAAGTTTCGTG 777
Db 781 TCATTGCAGATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
QY 778 TGACATGACGATGCTCTTTTGGCGTTTCATCTGGAATTCGGCCCTCTCGCGTGGCTCTCGAA 837
Db 841 TCCACTGATGATATCGTCACTGCTTTTCATCTGGAATCAGATTTCTCGAGCCGTTTATCT 900
QY 838 AGAATCGATGGCTCTGACCTACCGAGTTCTCGCGTGTCTGCGTGTCTGATGCTCGACCGCAATG 897
Db 901 CGACTTAAACCGAAGCAAAATCAAAATTTAGGCGGTGCTGATGTTAGAAAACGGCTA 960
QY 898 GGTGTCTCGAAACAACTACCCAGGCTTCTTCAAAACATGACCTTACCACAACTCGACCATC 957
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Db 961 GGACTCCCGAAACGATATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020  
Qy 958 GCGGAATCGCAACGAGTCACTCCGCGCAACAGCATCAGCGCTTCGTTTCAGAACTCGAC 1017  
Db 1021 AAAAGCTTGGATCATATAAAGTTTGGCGGTTCTTGCATCACAGATTCCGACGAGCTAGAC 1080  
Qy 1018 CCGCGGAGCA-----TGCGCCAGCGCAACAGAGGTCTCGCAGCTTACCTGACACAAAC 1071  
Db 1081 CTTAAAGTCTTCGATTGGCCCTATATACATGCGCACTTCTACGCTCTCTTAGCCGATGC 1140  
Qy 1072 CCGCAACGTCGAAGTATCCCTGACGCTGATGCGGACCAATCTACAGCGTCTATGCTG 1131  
Db 1141 CCGCAACGACTAAGGTTTCTATACCTCAACAAATTGATCTTATCTGGAATTATGCTG 1200  
Qy 1132 AGTCTTGGGCAAGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGGCC 1191  
Db 1201 AGTTCGTGGGCAAAAGTCAGCGCTGTATGACGTGATTTCAATCTAGGCTTGGGAGGCC 1260  
Qy 1192 GAGACTGTGAGACGGGCAATCTTTGAGCCTGTTGAGAGCTTGTATGATCTTTATGCCAAG 1251  
Db 1261 AAGAGTGTACGACGCGCGGCTTCATTTCCCTTGAGAGCTAATATATTTATGCTAGA 1320  
Qy 1252 AAGCCTGATGGCGAGTCTGTGGCGGCTTTCTCTGAGGGATGAGATGACCGATTG 1311  
Db 1321 TCTCCAGAGGTGAATGGTGGTGTCTCTTTGCTTTAGAGATAAAGATTGGGAGTGCCTG 1380  
Qy 1312 AAGCGGATAGGAGTGGACCAAGTATGC 1340  
Db 1381 AATGGGATAGGAATGGCAAAATATGC 1409

## RESULT 11

US-10-653-047-4594  
; Sequence 4594, Application US/10653047  
; Publication No. US20040229367A1

## GENERAL INFORMATION:

; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjørke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 5849, 200-US  
; CURRENT APPLICATION NUMBER: US/10/653, 047  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/533, 559  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/273, 623  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4594  
; LENGTH: 695  
; TYPE: DNA  
; ORGANISM: Aspergillus oryzae  
; FEATURE:

; NAME/KEY: misc\_feature  
; LOCATION: (1)...(695)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-653-047-4594

Query Match 10.8%; Score 146.2; DB 18; Length 695;  
Best Local Similarity 57.5%; Pred. No. 2.3e-39;  
Matches 325; Conservative 0; Mismatches 225; Indels 15; Gaps 3;  
Qy 5 CTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACAGCGCTTCCTTTCGATCTACACCC 64  
Db 109 CATTACATGTAAGCTGAACTTCTCTGGGTGAGTGTGCTGCTGCTC---AGGATCTACACGC 165  
Qy 65 AATACATCTCCTCTACCCCGTCTCTGATTCCTCTCAATATCCACTATTGTGACGACCT 124

Db 166 AAATCTGCTCTGCTTTCCGTTTC---GATGCTCATCTGTATCAAGAGATAGTCAAGACCC 222  
Qy 125 TCGACRAAGTCTTAAAGCGCTTCTCCGAAGCGCTGCCATGGGTGCGAGGCCAGGTCAAAG 184  
Db 223 TAGAGATGGCTCGAAGAGCTGTCCACCAATTTCCCGTGGGTAGCAGGCCAGATAGTCA 282  
Qy 185 CCGAGGGCATTTAGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGGAGGACGTTT 244  
Db 283 GTGAAGGCGAGCAGCCACAAACATCTGCGACATTCATGATCAAAAGCACTGGGGAAGACTC 342  
Qy 245 CTCGTGTTGTAGTAAGACCTCCGCGATGATCTTTCAGCGCCCAACGATCGAGGGTATGA 304  
Db 343 CACCACTGTTGTGAAGACTTCGCTCATGATCCGAGCTTCCGACCATGACGATTTGA 402  
Qy 305 GAAAGCGCGGATACCTTATGCGATGTTTGACGAGAACATCATCGCGCCAAAGGAAGAGCT 364  
Db 403 GACGCGCGAGCTTCCCTTTCCGATGTTAGAGAGAACATCATTTGCTCCTCGGAAACCT 462  
Qy 365 TACCTATTGGACCTGGTACTGTCCTCCGACGAGCCCAAGCCCTGTATTTCTATTGACGTCA 424  
Db 463 TGCCAA-----GCCCTGACGAAGATATATCTCACCGGCTTTCTTGTCCAGGCTA 513  
Qy 425 ACTTCATCAAGGGCGGACTCATCTCCTCACTGTCAACGGACAGACGCTGCTATGGATATGG 484  
Db 514 ATTNTATTACGCGCGGCTGCTGCTCCTCATCTTTGTGGCCATCATAGCAATGACATGA 573  
Qy 485 TAGGCAAGATGCGGTGATCCGCTCTACTCTCAAGCGGTGCGGTAAACGACCCATTCAACG 544  
Db 574 CTGGTCANGGACAGGTTATCCACCTTCTCTCGAAGGCATGCTGTTGGGATACATATACA 633  
Qy 545 AAGAGAAATGACGCCCATGAACCT 569  
Db 634 GATTGGAGCTAGAGTCAGGGAACCT 658

## RESULT 12

US-10-369-493-27681/C  
; Sequence 27681, Application US/10369493  
; Publication No. US2003033675A1

## GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369, 493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360, 039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 27681  
; LENGTH: 1947  
; TYPE: DNA  
; ORGANISM: Neurospora crassa  
US-10-369-493-27681

Query Match 2.9%; Score 39.2; DB 15; Length 1947;  
Best Local Similarity 53.2%; Pred. No. 0.055;  
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1050 CCGCAGCTACCTGCGACAAACCCCGACAAGTCCAAAGTATCCCTGACCGCTGATGCGGA 1109  
Db 1854 CCGCAGATAGCTGTCGCACACCAACGTCATGACAAACGTGTAAATGGCCGCTGTGGCGG 1795  
Qy 1110 CCCATCTACAGCTCATGCTGAGTCTTGGGCCAAGTGGGACTCTGGGATTCGACTT 1169  
Db 1794 CGCCTGGAACTCGCCTTCATGTTTGCATGCGAACGTCGCGCTCTTCCGCTCCGACTC 1735  
Qy 1170 TGGGCTCGGACTGGGTAAAGCCCGAGACTGTGAGACG 1205

Db 1734 GTAAATGGGCGCTGTCAAAGCTGACAAAGGTGAAGG 1699

RESULT 13

US-10-767-701-11710  
; Sequence 11710, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 11710  
; LENGTH: 688  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(688)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13347\_1  
US-10-767-701-11710

Query Match 2.7%; Score 36.4; DB 17; Length 688;

Best Local Similarity 47.4%; Pred. No. 0.31;  
Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 940 TACCACAACTCGAACCTCGCGGAAATCGCAACGAGTCACTCGCGCAACAGCATCACGC 999  
DB 20 TAAGTCACTACCCCTTGAGCTCCGGTCAGGCTGCTCAAGCTCAATTGTACTGTGT 79  
QY 1000 CTTGCTTCAAGATCGACCCCGGAGATCGCGGCAAGAGAGGTCTCGGAGGTAC 1059  
DB 80 CAGCGGAAGAAAGAGAGACACTCCAGCTCCGGGCTCCAGAGATCGAGCGCAAG 139  
QY 1060 CTGCACAAACCCGACAGTCCAGCTATCCCTGACGCTGATCGGACCCATCTACC 1119  
DB 140 ATGAAGAGGGCAACGCGAACTCGTCGACATCTATCGCCATCATCTCCCTCTC 199  
QY 1120 AGGCTCATGTGAGTTCTTGGGCAAGGTGGGACTCTGGGATTACGACTT 1169  
DB 200 GGGCTTCTTCAAGTTCGGCTGCAAGGTGAGTTCTGGCTCTGCTCTT 249

RESULT 14

US-10-767-701-11709  
; Sequence 11709, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 11709  
; LENGTH: 684  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13347\_2  
US-10-767-701-11709

Query Match 2.7%; Score 36.2; DB 17; Length 684;

Best Local Similarity 47.6%; Pred. No. 0.36;  
Matches 107; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 945 CAACTCGACCATCGCGGAAATCGCAACGAGTCACTCGCGCAACAGCATCACGCTTCG 1004  
DB 17 CCATCATCCCTTGGAGCTCCCGGTCAAGCTCAATTGTACTGTGTGTCAGCG 76  
QY 1005 TTCAGAACTCGACCCCGGAGCATGCGCGAGCAACAAAGGCTCTCGCGAGTACCTGCA 1064  
DB 77 GGAAGAAAGAGGAGACACCTCCAGCTCCGGGCTCCAGAGATCGAGCGCAAGATGAA 136  
QY 1065 CAACACCCCGACAGTCCAACTATCCCTGACGCTGATCGGAGCCCTCTACCGCT 1124  
DB 137 GGAGGCGACGGGCAACTGGCTGACATCTCATCGCATCATCTCCCTCTCTCGGCGT 196  
QY 1125 CATGCTGAGTTCTTGGGCCAAAGTGGGACTCTGGGATTACGACTT 1169  
DB 197 CTTCTCAAGTTCGGCTGCAAGGTGAGTTCTGGCTCTGCTCTT 241

RESULT 15

US-10-425-115-66302  
; Sequence 66302, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 66302  
; LENGTH: 1707  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_160468C.1  
US-10-425-115-66302

Query Match 2.7%; Score 36; DB 18; Length 1707;

Best Local Similarity 48.1%; Pred. No. 0.67;  
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 14 TACAGCTCGACACCTCGCGCAGCTACGAGGCTCTTTCGATCTACACCAATCAGTC 73  
DB 307 TCCGCGCTCCCTCCGCTCCACCTCCACTCGCTCCAGCCCAACCCCACTCCCTC 366  
QY 74 TCCTCTACCCCGTCTCTGATTCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAG 133  
DB 367 CCTACCGCTCGCTCTTCCGGCAGCGGAGGAGATCATCCGGAAGGGGGCGGAGACG 426  
QY 134 GTCTTAAGCGCTTCTCCGAAGCGGTCCCATGGTTCGAGGCCAGGTCAAAGCCGAGGCA 193  
DB 427 ACCTTCTCCCTCGGCGGGCGGAGGGGAGGAGGCGAGGCGGATGGTGGGGCG 486  
QY 194 TTAGCGGGAACACACAGGAATCTCTTATC 225  
DB 487 AGGGCGACGCGAGCGAGGCGGACTCGGTCAAC 518

Search completed: January 23, 2005, 19:45:39  
Job time : 825 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 13:23:58 ; Search time 138 Seconds  
(without alignments)  
6984.273 Million cell updates/sec

Title: US-10-614-954-5  
Perfect score: 1356  
Sequence: 1 atgggtttcaagatacagct.....atgcgacgttggttag 1356

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*
- 2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/PCUTUS COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	3	US-09-538-414-5
2	1356	100.0	1356	4	US-10-074-279-5
3	915.6	67.5	1403	3	US-09-538-414-1
4	915.6	67.5	12949	3	US-10-074-279-1
5	915.6	67.5	12949	3	US-09-538-414-11
6	915.6	67.5	12949	4	US-10-074-279-11
7	915.6	67.5	13737	3	US-09-538-414-10
8	915.6	67.5	13737	4	US-10-074-279-10
9	249.8	18.4	1425	3	US-09-538-414-7
10	249.8	18.4	1425	4	US-10-074-279-7
11	39.8	2.9	4403765	3	US-09-103-840A-2
12	39.8	2.9	4411529	3	US-09-103-840A-1
13	36.6	2.7	834	4	US-09-621-976-2574
14	34.2	2.5	720	4	US-09-252-991A-16032
15	34.2	2.5	1074	4	US-09-252-991A-16568
16	34.2	2.5	2721	4	US-09-252-991A-16144
17	34	2.5	1713	4	US-09-540-236-1014
18	34	2.5	269223	4	US-09-596-002-41
19	33.4	2.5	516	4	US-09-252-991A-15293
20	33.4	2.5	1614	4	US-09-252-991A-15438
21	33.2	2.4	399	4	US-09-621-976-8976
22	33	2.4	832	4	US-09-621-976-2813
23	32.8	2.4	1230025	4	US-09-198-452A-1
24	32.4	2.4	1620	3	US-09-125-642C-9
25	32.4	2.4	1740	3	US-09-125-642C-2
26	32.4	2.4	1742	3	US-09-125-642C-13
27	32.4	2.4	5515	3	US-09-125-642C-8

ALIGNMENTS

RESULT 1

US-09-538-414-5  
; Sequence 5, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-09-538-414-5

Query Match	100.0%;	Score 1356;	DB 3;	Length 1356;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGAGCCCTCCTTTTCGATCTAC	60	
Db	1	ATGGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGAGCCCTCCTTTTCGATCTAC	60	
QY	61	ACCCAATCAGTCTCCTCTTACCCCGCTCTGATTTCTCTCAATATCCCACTATTTGTCAGC	120	
Db	61	ACCCAATCAGTCTCCTCTTACCCCGCTCTGATTTCTCTCAATATCCCACTATTTGTCAGC	120	
QY	121	ACCTTCGACACAGCTTTAAGCGCTTCTCGAAGCCGTCCTCGAGCCGTCGAGCCGAGGTC	180	
Db	121	ACCTTCGACACAGCTTTAAGCGCTTCTCGAAGCCGTCCTCGAGCCGTCGAGCCGAGGTC	180	
QY	181	AAAGCCGAGGCGATTAGCGAGGAAACACAGAACTTCTTTTATCGTCCCTTTTGAGGAC	240	
Db	181	AAAGCCGAGGCGATTAGCGAGGAAACACAGAACTTCTTTTATCGTCCCTTTTGAGGAC	240	
QY	241	GTTCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGCCACGATCGAGGCT	300	
Db	241	GTTCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGCCACGATCGAGGCT	300	
QY	301	ATGAGAAAGCGCGGATACCCCTATGGCGATGTTTGAGGAGAACATCATCGGCCCAAGAG	360	
Db	301	ATGAGAAAGCGCGGATACCCCTATGGCGATGTTTGAGGAGAACATCATCGGCCCAAGAG	360	

Db 301 ATGAGAAAGCGGGATACCTATGCGATGTTTGAACGAGAAATCATATCGGCCAAGGAAG 360  
QY 361 ACCTTACCTATTGACCTGCTACTGCTCCGACGACCCAAAGCCTGTAATCTTATTGACG 420  
Db 361 ACCTTACCTATTGACCTGCTACTGCTCCGACGACCCAAAGCCTGTAATCTTATTGACG 420  
QY 421 CTCAACTTCATCAAGGCGGACCTCACTCTCACTGTCAACGAGCAGCACGGTCTATGGAT 480  
Db 421 CTCAACTTCATCAAGGCGGACCTCACTCTCACTGTCAACGAGCAGCACGGTCTATGGAT 480  
QY 481 ATGGTAGGCAAGATCGGCTGATCGCTCTACTCTCAAGCGCTGCGTAACACCCATTC 540  
Db 481 ATGGTAGGCAAGATCGGCTGATCGCTCTACTCTCAAGCGCTGCGTAACACCCATTC 540  
QY 541 ACCGAGAGGAATATGACGCGCATGAACTTCGATCGCAAGACGATAGTCTCTTACCTTGA 600  
Db 541 ACCGAGAGGAATATGACGCGCATGAACTTCGATCGCAAGACGATAGTCTCTTACCTTGA 600  
QY 601 AACTATACGATTGGCCCGGAGTATCATCATAGATTGTCAAAAGCTGATAGTCTGTGT 660  
Db 601 AACTATACGATTGGCCCGGAGTATCATCATAGATTGTCAAAAGCTGATAGTCTGTGT 660  
QY 661 GACGCTGTTCTACGCGCGTCAAGTCAAGTGGGCGTCTTCAATTCAGCCCAAGGCC 720  
Db 661 GACGCTGTTCTACGCGCGTCAAGTCAAGTGGGCGTCTTCAATTCAGCCCAAGGCC 720  
QY 721 ATGTACAGCTCAAGATGCTGCTCAACAGACTCTTGAAGCATCAACAAAGTTCGTGTG 780  
Db 721 ATGTACAGCTCAAGATGCTGCTCAACAGACTCTTGAAGCATCAACAAAGTTCGTGTG 780  
QY 781 ACTGACGATGCTCTTTTCCGCGTTTCACTGGAATCGGCGCTCTCGGTGCGTCTCGAAGA 840  
Db 781 ACTGACGATGCTCTTTTCCGCGTTTCACTGGAATCGGCGCTCTCGGTGCGTCTCGAAGA 840  
QY 841 ATCGATGGCTTCGACCTACCGAGTTCGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900  
Db 841 ATCGATGGCTTCGACCTACCGAGTTCGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900  
QY 901 GTCTCGAAACAACTPACCCAGCGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 960  
Db 901 GTCTCGAAACAACTPACCCAGCGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 960  
QY 961 GAAATCGCCAAACGAGTCACTCGCGGCAACAGCATCAAGCATCAAGCTCGAATCGACCC 1020  
Db 961 GAAATCGCCAAACGAGTCACTCGCGGCAACAGCATCAAGCATCAAGCTCGAATCGACCC 1020  
QY 1021 GCGAGCATGCGCCAGCGAACAAGAGTCTCGGACGTAAGTCTGCAACCAACCCCGACAAG 1080  
Db 1021 GCGAGCATGCGCCAGCGAACAAGAGTCTCGGACGTAAGTCTGCAACCAACCCCGACAAG 1080  
QY 1081 TCCAAAGTATCCCTGACGGCTGATGCGGACCATCTACAGCGTCAATGCTGAGTCTTGG 1140  
Db 1081 TCCAAAGTATCCCTGACGGCTGATGCGGACCATCTACAGCGTCAATGCTGAGTCTTGG 1140  
QY 1141 GCCAAGTGGGACTCTGGGATACGATTTGGGCTCGGATGGGTAAGCCCGAGACTGTG 1200  
Db 1141 GCCAAGTGGGACTCTGGGATACGATTTGGGCTCGGATGGGTAAGCCCGAGACTGTG 1200  
QY 1201 AGACGGCAATCTTTGAGCTGTTGAGAGTCTGATGCTATCTTATGCCAAGAGCCTGAT 1260  
Db 1201 AGACGGCAATCTTTGAGCTGTTGAGAGTCTGATGCTATCTTATGCCAAGAGCCTGAT 1260  
QY 1261 GCGAGTCTGTCGGCGCTTCTCTGAGGATGAGGATATGACCGATGAGGCGGAT 1320  
Db 1261 GCGAGTCTGTCGGCGCTTCTCTGAGGATGAGGATATGACCGATGAGGCGGAT 1320  
QY 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356  
Db 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356

; Sequence 5, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-10-074-279-5

Query Match 100.0%; Score 1356; DB 4; Length 1356;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTCGATCTAC 60  
Db 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTCGATCTAC 60  
QY 61 ACCCAATACAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGACG 120  
Db 61 ACCCAATACAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGACG 120  
QY 121 ACCTTCGAGCAAGTCTTAAAGCGCTCTCCGAGCGCTCCCATGGTGCAGGCCAGGTC 180  
Db 121 ACCTTCGAGCAAGTCTTAAAGCGCTCTCCGAGCGCTCCCATGGTGCAGGCCAGGTC 180  
QY 181 AAAGCCGAGGGCATTTAGCGAGGAAACACAGAACTTCTTTATCGTCCCTTTTCAGGAC 240  
Db 181 AAAGCCGAGGGCATTTAGCGAGGAAACACAGAACTTCTTTATCGTCCCTTTTCAGGAC 240  
QY 241 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTACGCGCCACGATCGAGGT 300  
Db 241 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTACGCGCCACGATCGAGGT 300  
QY 301 ATGAGAAAGCGCGGATACCTATGCGATGTTTGAAGAACATCATCGGCCAAGGAAG 360  
Db 301 ATGAGAAAGCGCGGATACCTATGCGATGTTTGAAGAACATCATCGGCCAAGGAAG 360  
QY 361 AGTTACCTATTGGACCTGTTACTGCTCCGACGACCCAAAGCCTGTAATCTTATTGACG 420  
Db 361 AGTTACCTATTGGACCTGTTACTGCTCCGACGACCCAAAGCCTGTAATCTTATTGACG 420  
QY 421 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGAGCAGCACGGTCTATGGAT 480  
Db 421 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGAGCAGCACGGTCTATGGAT 480  
QY 481 ATGGTAGGCAAGATCGGCTGATCGCTCTACTCTCAAGCGCTGCGTAACACCCATTC 540  
Db 481 ATGGTAGGCAAGATCGGCTGATCGCTCTACTCTCAAGCGCTGCGTAACACCCATTC 540  
QY 541 ACCGAGAGGAATATGACGCGCATGAACTTCGATCGCAAGACGATAGTCTCTTACCTTGA 600  
Db 541 ACCGAGAGGAATATGACGCGCATGAACTTCGATCGCAAGACGATAGTCTCTTACCTTGA 600  
QY 601 AACTATACGATTGGCCCGGAGTATCATCATAGATTGTCAAAAGCTGATAGTCTGTGT 660  
Db 601 AACTATACGATTGGCCCGGAGTATCATCATAGATTGTCAAAAGCTGATAGTCTGTGT 660  
QY 661 GACGCTGTTCTACGCGCGTCAAGTCAAGTGGGCGTCTTCAATTCAGCCCAAGGCC 720

Db 661 GACGCTGTTCTCAAGCGGTCAGTGAAGCTGGGCGTCTTTCACATTCAGCCCCAAGGCC 720  
Qy 721 ATGTCAAGCTCAAGATGCTGTACCAAGATCTTTGAGCGATCAACAAGTTGGTGG 780  
Db 721 ATGTCAAGCTCAAGATGCTGTACCAAGATCTTTGAGCGATCAACAAGTTGGTGG 780  
Qy 781 ACTGACGATGCTCTTTTCGGGCTTCATCTGGAATCGGCTCTCGGTGCTCGAAGA 840  
Db 781 ACTGACGATGCTCTTTTCGGGCTTCATCTGGAATCGGCTCTCGGTGCTCGAAGA 840  
Qy 841 ATCGATGGCTCTGCACCTACCGATGTTCTGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900  
Db 841 ATCGATGGCTCTGCACCTACCGATGTTCTGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900  
Qy 901 GTCTCGAACAATCACTACCGGCTCTTCAAAACATGACCTACCAAACTCGACCATCGGC 960  
Db 901 GTCTCGAACAATCACTACCGGCTCTTCAAAACATGACCTACCAAACTCGACCATCGGC 960  
Qy 961 GAAATCGCAACAGTCACTCGGCGCAACAGCATCAAGCTTCTGTTTCAAACTCGACCCC 1020  
Db 961 GAAATCGCAACAGTCACTCGGCGCAACAGCATCAAGCTTCTGTTTCAAACTCGACCCC 1020  
Qy 1021 GCGAGCATCGGCGCAACAGGCTCTCGGAGCTTCTGCGAGCTACGACCAACCCCGAAG 1080  
Db 1021 GCGAGCATCGGCGCAACAGGCTCTCGGAGCTTCTGCGAGCTACGACCAACCCCGAAG 1080  
Qy 1081 TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTACAGGCTCATGCTGAGTCTTGG 1140  
Db 1081 TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTACAGGCTCATGCTGAGTCTTGG 1140  
Qy 1141 GCCAAGTGGGACTCTGGGATTAAGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200  
Db 1141 GCCAAGTGGGACTCTGGGATTAAGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200  
Qy 1201 AGACGGCCAACTTTGAGGCTGTGAGGCTGATGATCTTTATGCGGAGAGGCTGAT 1260  
Db 1201 AGACGGCCAACTTTGAGGCTGTGAGGCTGATGATCTTTATGCGGAGAGGCTGAT 1260  
Qy 1261 GCGAGTCTGTGCGGCTTTCTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1320  
Db 1261 GCGAGTCTGTGCGGCTTTCTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1320  
Qy 1321 AAGGAGTGACCAAGTATGCGAGTACGTTGGTTAG 1356  
Db 1321 AAGGAGTGACCAAGTATGCGAGTACGTTGGTTAG 1356

RESULT 3  
US-09-538-414-1  
; Sequence 1, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1403  
; TYPE: DNA  
; ORGANISM: Fusarium sporotrichioides  
US-09-538-414-1

Query Match 67.5%; Score 915.6; DB 3; Length 1403;

Best Local Similarity 80.3%; Pred. No. 1.1e-283;  
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;  
Qy 3 GGTCTTCAAGATACAGCTCGACACCTCGGCGAGCTTACAGGCTCTCTTTTCATCTACAC 62  
Db 36 GTCTTTTGCATAGAGCTCGACATCATCGGCGAGCAACGCGCTCTCTTTTCATCTACAC 95  
Qy 63 CCAATTCAGTCTCTTACCCGCTCTCTGATTTCTCTCAATATCCACATTTGTTCAGCAC 122  
Db 96 CCAGATCAGTCTCTTACCCGCTCTCTGATCCCTCCAGATCCACCATCGTCAGCAC 155  
Qy 123 CTTGAGCAGGCTCTTAAAGGCTTCTCGAAGCGCTTCCATGGGTGCGAGGCGGCTCAA 182  
Db 156 CTTGAGGAGGCGCTTAAAGCGCTCTCTCAAACTTCCCATGGGTGCGGCGGCGAGGTCAA 215  
Qy 183 AGCCGAGGCGCTTAAAGCGGGAACACAGGAACTCTCTTTTATCTGCTCTCTTTTGAAGACGT 242  
Db 216 GACCGAGGCGCTTAAAGCGGGAACACAGGAACTCTCAAGATCATTTCCATATGAGGAGAC 275  
Qy 243 TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTTCAGGCGCCACGATCGAGGCTAT 302  
Db 276 ACCCGCTCTTGTGGTGAAGACCTCGTGTATGATCTCTCAGGCGCAACGATCGAGGCTT 335  
Qy 303 GAGGAGGCGGCTTACCTATGCGGATGTTTTCAGGAGACATCATCGCGCGAGGAGAC 362  
Db 336 GAGGAGGCGGCTTACCTATGAGATGTTTTCAGGAGACCTCGTCTCGGAGGAGAC 395  
Qy 363 GTTACCTATTGACCTTGGTACTTGGTCTCCGACCAACCAAGCTGTAACTTCTATTGACGCT 422  
Db 396 ATTAGTATCGACCTTGGCAATGGCCCCAAGCGGAGCTGTGTGCTATTGAGCT 455  
Qy 423 CAACTTCATTAAAGGCGGACTCATCTCACTGTCAACGAGACGAGCTGTGTGATAT 482  
Db 456 CAACTTCATTAAAGGCGGACTCATCTCACTGTCAACGAGACCAACATGCTGTATGACAT 515  
Qy 483 GGTAGGCGGAGTGGGTGATCGGTCTACTCTCAAGGCTGCGGTAAAGCCGATTCAC 542  
Db 516 GACGAGCAAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 575  
Qy 543 CGAAGGAGAAATGACGCGCATGAACCTCGATCGAAGACGATAGTTCCTTATCCTTGAAGA 602  
Db 576 CGAGGAGGAAATCTCGGCACTGAACCTCGATCGAAGACGAGTATGCTCTCTTGAAGA 635  
Qy 603 CTATAGATGTCGCCCGAGGTAGATCATCAGATGTCAAAGCTGTGTAGCTGTGTGTA 662  
Db 636 CTACAAAGTTGCTCTGAGCTAGACCAACAGATCGCAAAACCC---TGCGCTGCTGCGCA 692  
Qy 663 CGCTGTTCTACGCGGCTCAGTGAAGCTGGGCTTCTTCAATTCAGGCGCCCAAGGCTAT 722  
Db 693 CGCTCCACCGGCGCAAGGCTGGGCTTCTTCAATTCAGGCGCCCAAGGCTAT 752  
Qy 723 GTGAGGCTCAAGGATGCTGTACCAAGACTCTTGACGATCAACAAAGTTCTGTGTGAC 782  
Db 753 CTGAGGCTGAAGACGAGCGCAACAGACTCTTGACGCTGTGTGCTGTGTGCTCAAC 812  
Qy 783 TGAAGATGCTCTTTTCGGGCTTCACTGGAATTCGGGCTCTCGGCTGTGTGCTGTGTAAGAAT 842  
Db 813 TGATGATGCTCTTTTCGGGCTTCACTGGAATTCGGGCTCTCGGCTGTGTGCTGTGTAAGAAT 872  
Qy 843 CGATGGCTCTGACCTACCGGCTTCTGCGGCTGTGTGATGCTGACCGGCGGCTATGGGTGT 902  
Db 873 GGATGCTTCCACACCTTCTGGAATTCGCGGCTGTGTGATGCTGACCGGCGGCTATGGGCT 932  
Qy 903 CTGGAACACTTACCGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGCGCA 962  
Db 933 ATCAAGCATATACCGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGCGCA 992  
Qy 963 AATCGCCAAAGCTCACTCGGCGCAACAGCATCAAGCTTGTGCTGTGCTGTGCTGTGCTGTG 1022  
Db 993 AATCGCCAAAGCACTTGGCGCAACAGCATCAAGCTTGTGCTGTGCTGTGCTGTGCTGTG 1052  
Qy 1023 GAGCATGCGCGAGGCAAGAGGCTCTCGGAGGTCTCGGAGGTCTGTGCAACCAACCCGAGAGTC 1082



Db	1053	TCGTTTGGCGACAGCAACAAAGCTTTTGGCGAGCTAGATGATGCGCTGCTGACAGTC	1112
Qy	1083	CAACGTATCCCTGACGGCTGATGCGACCCATCTACAGCGTCACTGAGTTCCTGGGC	1142
Db	1113	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTTCCTGGGC	1172
Qy	1143	CAAGTGGGACCTCTGGGATAGACATTTGGGCTCGGACTGGTAAGCCCGAGACTGTGAG	1202
Db	1173	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGGTAAAGCCTGAGTGTGAG	1232
Qy	1203	ACGGCCAACTTTGAGCGCTTGGAGCTTGGAGCTTGTATGTTATGTCCTCAAGAACCTGTATGG	1262
Db	1233	AAGACTCCCTTGAACCTTTTGAAGTTGATGACTTTATGTCCTCAAGAACCTGTATGG	1292
Qy	1263	CGAGTTCTCTGGGGCGCTTTCTCTGAGGATGAGGATATGGAACCGAATGAGCGCGATAA	1322
Db	1293	GGAGTTTACGGCTCCATTTCTCTGAGGATGAGGATATGGAACCGAATGAGCGCGATAA	1352
Qy	1323	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	1353	GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG	1386
RESULT 4			
US-10-074-279-1			
; Sequence 1, Application US/10074279			
; Patent No. 6646184			
; GENERAL INFORMATION:			
; APPLICANT: Hohn, T.			
; APPLICANT: Salmeron, J.			
; APPLICANT: Peters, C.			
; APPLICANT: Kendra, D.			
; APPLICANT: Reindars, J.			
; APPLICANT: Kuznia, R.			
; APPLICANT: Dill-Mackey, R.			
; TITLE OF INVENTION: Transgenic Plant and Methods			
; FILE REFERENCE: sequencelist			
; CURRENT APPLICATION NUMBER: US/10/074,279			
; CURRENT FILING DATE: 2002-02-12			
; PRIOR APPLICATION NUMBER: US/09/538,414			
; PRIOR FILING DATE: 2000-03-29			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 1403			
; TYPE: DNA			
; ORGANISM: Fusarium sporotrichioides			
US-10-074-279-1			
Query Match 67.5%; Score 915.6; DB 4; Length 1403;			
Best Local Similarity 80.3%; Pred. No. 1.1e-283;			
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
Qy	3	GGCTTCAAGATACAGCTGACACCCCTCGGCGAGCTACAGGCTCGTTTCGATCTACAC	62
Db	36	GTCTTTTGACATAGAGCTGACATCATCGGCGACGACACCGCTCTTTTCAATCTACAC	95
Qy	63	CCAAATCAGTCTCTTACCCCGTCTGATTCCTCTCAATATCCCACTATTGTTCAGCAC	122
Db	96	CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCACTATCGTCAGCAC	155
Qy	123	CTTCGACCAAGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTGCGACGCGAGTCAA	182
Db	156	CTTTGAGGAAGGCTAAAGCCCTCTCTCAACCTTCCCATGGGTGCGGCGCCAGGTCAA	215
Qy	183	AGCGAGGGCTATTAGCGAGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAAGGACGT	242
Db	216	GACCGAGGGCATCAGCGAGGAACACAGGAACCTTCGAAGTATTCATATGAGGAGAC	275
Qy	243	TCCTCGTCTGTAGTGAAGACCTCCGCGATGATCTTTACGCGCCACGATCGAGGGTAT	302
Db	276	ACCCGCTCTGTGGTGAAGACCTCCGCTGATGATTCCTCAGCGCCAAAGATCGAGGGGTT	335



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RESULT 5
US-09-538-414-11
; Sequence 11, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-09-538-414-11

Query Match      67.5%; Score 915.6; DB 3; Length 12949;
Best Local Similarity 80.3%; Pred. No. 4e-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GCGTTTCAAGATACAGCTCGACACCTCGGCGAGCTACCAAGGCTCCTTTTCATCTACAC 62
DB 11281 GTCCTTTGATAGAGCTGACATCATCGGCGAGCAACCGCTCTCTTTCAATCTACAC 11340
QY 63 CCAATACAGTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCAC 122
DB 11341 CCAGATCAGTCTGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 11400
QY 123 CTTTCAGAGCAAGGTCTTAAGCGTCTTCCGAAGCGTCCCATGGTCCGAGCGCAGGTCAA 182
DB 11401 CTTTCAGAGCAAGGTCTTAAGCGTCTTCTCAAACTTCCCATGGTCCGCGCGCAGGTCAA 11460
QY 183 AGCGGAGGCAATTAGCGAGGGAACACAGGAATCTCTTTATGTCCTCTTTTGGAGACGT 242
DB 11461 GACCGAGGCAATCAGCGAAGGAACACAGGAATCTTCCAGATCATTTCCATATGAGGAGAC 11520
QY 243 TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTTCCAGCGCCCAAGATCGAGGCTAT 302
DB 11521 ACCCGCTGTGTGTTGAAGACCTCCGCGATGATCTTCCAGCGCCCAAGATCGAGGCTAT 11580
QY 303 GAGAAAGCGGGATACCTTATGGCGATGTTTGAAGAGACATCATCGCGCCCAAGGAAGAC 362
DB 11581 GAGAAAGCGGGATACCTTATGGCGATGTTTGAAGAGACATCATCGCGCCCAAGGAAGAC 11640
QY 363 GTTACCTATTGACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 422
DB 11641 ATTAGCTATCGGACCTTGGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 11700
QY 423 CAACCTTCAAGGCGGACTCATCTCTCATCTGTCAACGGACAGCAGCGTCTATGATAT 482
DB 11701 CAACCTTCAAGGCGGACTCATCTCTCATCTGTCAACGGACAGCAGCGTCTATGATAT 11760
QY 483 GGTAGGCCAAGATGCGGTGATCGTCTATCTTCAAGGGGTGCGGTAAAGCAACCATTCAC 542
DB 11761 GACAGGACAAGATGCAATATTGCTCTTCTTCAAGGGGTGCGGTAAAGCAACCATTCAC 11820
QY 543 CGNAGGGAATGACGCCCATGACCTCGATCGCAGAGCAGTAGTTCCTTACCTTGAA 602
DB 11821 CGAGGAGGAATGACGCCCATGACCTCGATCGCAGAGCAGTAGTTCCTTACCTTGAA 11880
QY 603 CTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAAGCTGATGTAGTGGTGA 662
DB 11881 CTAAAGATTGGTCTGAGCTAGACCAACCATGCGCAACAC---TGGCGTGTGCGCA 11937
QY 663 CGCTGTTCTACGCGCGGTGAGTCAAGCTGGGCGTTCTTTCATATTCAGCCCCCAAGGCCAT 722

RESULT 6
US-10-074-279-11
; Sequence 11, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

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723 GTCCAGAGCTCAAGGATGCTGTCTACCAAGACTCTTGACGCATCAACAAAGTTTCGTGTGAC 782
11998 CTGGAGCTGAAGAGCGCAGCCACCAAGACTCTTGACGGGTGCTCCAAAGTTTGTGTCAAC 12057
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12058 TGATGATGCTCTTTTCGGCGTTCATCTGGAATTCGGGCTCTCGGTCGCTCTGCAAGAT 12117
843 CGATGCTCTGACCTACCGAGTTCCTGCGTCTGTTGATGCTCGACCGGCAATGGGTGT 902
12118 GGATGCTTCCACACTTACTGAAATTCGCGCGCTGTGCAATGCGGGGCGCCCAATGGGCGT 12177
903 CTCGAACACTTACCCAGGCTCTTCTCAAAACATGACCTACCAACATCGACCATCGGCCA 962
12178 ATCAAGCACAATACCCAGGCTCTTCTCAAAACATGACCTACCAACATCGACCATCGGCCA 12237
963 AATCGCCAAACGAGTCACTCGGCGCAACAGCATCAAGCTTCGTTCAAGACTCGACCCCGC 1022
12238 AATCGCCAAACGAAACCACTTGGCGCAACAGCATCAAGCTTCGCGCTCGAACTCAACAGTGA 12297
1023 GAGCATGCGCCAGCAAGAGGCTCTCGGAGCTACCTGCAACCAACCCCGCAAGTC 1082
12298 TCGTTTGGCGCAGCAACCAAGCTTTTGGCGAGCTACATGSCATGGCTCGCTGACAAATC 12357
1083 CAAAGTATCCCTGAGCGGTGATGCGGACCCATCTACACGCTCATCTGAGTTCTTGGGC 1142
12358 GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAGCAGCATCATGCTGATGTTCTGGGC 12417
1143 CAAAGTGGGACTCTGGAATTACGATTTTGGGCTCGGACTGAGTAAAGCCGAGACTGTGAG 1202
12418 CAAAGTGGGACTCTGAGGATGATGACTTTGGGTTTGGACTGAGCTGAGAGTGTGAG 12477
1203 AGGCGCAATCTTTGAGCTGTTGAGAGCTGATGATCTTTATGCCCAAGAGCTGATGG 1262
12478 AAGACTCTGCTTGAACCTTTTGGAGGTTGATGATCTTTATGCCCAAGAGCTGATGG 12537
1263 CGAGTCTCTGCGCGCTTTCTCTGAGGATGAGATATGAGCCGATTCGAAGCGGATAA 1322
12538 GAGTTTACGGGCTCCATTTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGA 12597
1323 GAGTGGACCAAGATGCGCAGTACGTTGGTTAG 1356
12598 GAGTGGACCAAGTACGCAAGATATATTGGTAG 12631
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Query Match 67.5%; Score 915.6; DB 4; Length 12949;
Best Local Similarity 80.3%; Pred. No. 46-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GCGTTTCAGATACAGCTCGACACCTCGCGCAGCTACAGCCCTCCCTTTTCGATCTACAC 62
DB 11281 GTCTTTTGATAGAGCTCGATCATATCGCGCAGCAACCGCTCTCTTTTCAATCTACAC 11340
QY 63 CCAAAATCAGTCTCTTACCCCGTCTCTGATTTCTCTCAATATCCCATTTTGTGAG 122
DB 11341 CCAGATCAGTCTCTGTTTACCCCGTCTCTGATCCCTCCAGATCCCATCGTCAGCAC 11400
QY 123 CTTTCGAGCAAGGTCTTAAAGGCTTCTCGAAGCGCTCCCATGGTTCGAGCGCAGTCAA 182
DB 11401 CCTTGAGGAAGGCTTAAAGGCTTCTCTCAAAACCTTCCCATGGTTCGCGGGCCAGTCAA 11460
QY 183 AGCGGAGGCAATPAGCGAGGAAACACAGAACTTCTCTTATCTGCTCCCTTTTGAAGAGCT 242
DB 11461 GACCGAGGCGCATCAGCGAAGGAACACAGAACTTCCAGATCATTTCCATATGAGGAGAC 11520
QY 243 TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCCAGCGCCCAAGATCGAGGGTAT 302
DB 11521 ACCCGCTTGTGTGAAGACCTCGGTGATGATCTCTCAGCGCCCAAGATCGAGGGGT 11580
QY 303 GAGAAAGCGGGATACCTTATGCGATGTTTGAAGAGACATCATCGCGCCCAAGGAAGAC 362
DB 11581 GAGAAAGCGGGTTCCTCCCTTGAAGATGTTTGAAGAGACATCGTCTCGCTCCAGGAGAC 11640
QY 363 GTTACCTATTGACCTGTGTTACTCGTCCCGACGACCCAAAGCCCTGTAAATTTCTATTGAGCT 422
DB 11641 ATTAGCTATCGACTTGGCAATGCGCCCAAGACCCGAGCCCTGTGTCTATTGAGCT 11700
QY 423 CAACCTTCATCAAGGGGAGCTCATCTCTACTGTCTCAACGAGACACGCTGTCTATGATAT 482
DB 11701 CAACCTTCATTAAGGGGAGCTCATCTCTACTGTCTCAACGAGACACATGCTGTCTATGACAT 11760
QY 483 GGTAGGCAAGATCGGGTGTGCTGCTTACTCTCAAGGGTGGTGAAGACCCATTTAC 542
DB 11761 GACAGGCAAGATGCAATTTCTGCTCTCTCTCAAGGGTGGTGAAGACCCATTTAC 11820
QY 543 CGAAGAGAAATGACGGCCATGAACCTCGATCGACGACGATAGTTCCTTACCTTGAA 602
DB 11821 CGAGGAGAAATCTCGGCCATGAACCTCGATCGACGACGATAGTTCCTTCTCTTGAA 11880
QY 603 CTATACGATTTGCGCCCGAGGATGATCATGATGTTGATGATGATGATGATGATGATG 662
DB 11881 CTACAAAGTTGCTCTGAGCTAGACACCGAGTGCACAAACCTCTCTCTCTGCGG 11937
QY 663 CGCTGTTCTACGCGGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 722
DB 11938 CGCTCCACCGCCACCGCCAGGCAAGCTGCGGCTCTCTTCTTCTTCTTCTTCTTCTTCT 11997
QY 723 GTCAGAGCTCAAGGATGCTGTACCAAGCTCTTTCAGCGATCAACAAAGTTGCTGTGAC 782
DB 11998 CTCGAGCTGAAGACGAGCAGCACAAGAGCTCTTTCAGCGCTGCTGCTGCTGCTGCTG 12057
QY 783 TGACGATGCTCTTTCGGGCTTCTGCAATCGGCTCTGCGTGTGCTGCTGCTGCTGCTGCT 842
DB 12058 TGATGATGCTCTTTCGGGCTTCTGCAATCGGCTCTGCGTGTGCTGCTGCTGCTGCTG 12117
QY 843 CGATGGCTCTGCACCTACGAGTGTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
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QY 903 CTCGAACTACCTCAGGCTCTTTCAGAACTGACATGACCTACCACTGACCTGCGGCA 962
DB 12178 ATCAAGCATATACCGAGGCTTCTTCAAAACATGACCTTACCATGACCTGCGGCA 12237
QY 963 AATCGCAACAGTCACTCGCGCAACAGCATCAGGCTTCTGTTTCAAGAACTTCGACCCG 1022
DB 12238 AATCGCAACAGTCACTTTCGCGCAACAGCATCAGGCTTCTGTTTCAAGAACTTCAGTGA 12297
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12298 TCGTTTGGCAGACGAAACAAGCTTTGGCGAGTACATGCTGCGCTGCTGCAAGTC 12357
1083 CAAGTATCCCTGACCGCTGATCGGACCATCTACAGCGTCACTGCTGAGTTCTTGGGC 1142
12358 GAGCGTCTCCCTGACCGCGATCGAATCGGTCAAGCAGCATCATGCTGAGTTCTTGGGC 12417
1143 CAAGTGGGACTCTGGGATTAACGACTTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAG 1202
12418 CAAGTGGGATCTGGGAGTATGACTTTGGTGGGTTGGAGTGGTAAAGCTGAGAGTGTGAG 12477
1203 ACGCCCAATCTTGAAGCTGTGAGAGCTGTGAGTGTACTTTATGCCCAAGAGCCTGATGG 1262
12478 AAGACCTCGCTTGAACCTTTTGAAGTGTGATTTATGCTCCCAAGAGCCTGATGG 12537
1263 CGAGTTCTGTGCGCGCTTTCTCTGAGGATGAGGATATGAGCGATTGAAGCGGATAA 1322
12538 GGAGTTTACCGCGCTCAATTTCTCTGAGGATGAGGATATGAGGAGACTAAAGCGGATGA 12597
1323 GGAGTGAACCAAGTATGCGCAGTACGTTGGTTAG 1356
12598 GGAGTGGACAAAGTACGCAAGTATATTTGGGTAG 12631

RESULT 7
US-09-538-414-10
; Sequence 10, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; US-09-538-414-10

Query Match 67.5%; Score 915.6; DB 3; Length 13737;
Best Local Similarity 80.3%; Pred. No. 41e-283;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GCGTTTCAGATACAGCTCGACACCTCGCGCAGCTACAGCCCTCCCTTTTCGATCTACAC 62
DB 50 GTCTTTTGATAGAGCTCGACATCATCGCGCAGCAACCGCTCTCTTCAATCTACAC 109
QY 63 CCAAAATCAGTCTCTCTTACCCCGTCTCTGATTTCTCTCAATATCCCATTTTGTGAGCAC 122
DB 110 CCAGATCAGTCTGTTTACCCCGTCTCTGATCCCTCCAGTATCCCATCATGTCAGCAC 169
QY 123 CTTTCGAGCAAGGTCTTAAAGGCTTCTCGAAGCGCTCCCATGGTTCGAGCGCAGGTCAA 182
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QY 183 AGCGGAGGCAATPAGCGAGGAAACACAGAACTTCCAGAACTTCCATATGAGGAGAC 242
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QY 243 TCCTCGTGTGTAGTGAAGACCTCGCGCATGATCTTTCAGGCCCAAGTATCGAGGTAT 302
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Db 290 ACCCGCTTTGTGGTGAAGACCTCGTGATGATTCCTCAGCGCCAAACGATCGAGGGGTT 349  
Qy 303 GAGAAAGCGGGATACCCCTATGCGGATGTTTGACGAGAAACATCATCGCGCCCAAGGAAGAC 362  
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Qy 483 GGTAGGCCAAGATGCGGGTATCCGCTACTCTCAAGGGGTGCGGTAACGACCCATTTCAC 542  
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Qy 543 CGAGAGGAAATGACCGCCATGAACCTCGATCGCAAGCGGTGCGGCAACGAATCATTCAC 602  
Db 590 CGAGGAGGAAATGACCGCCATGAACCTCGATCGCAAGCGGTGCGGCAACGAATCATTCAC 649  
Qy 603 CTATACGATTTGCCCCGAGGTAGATCATCAGATTTGCAAGCTGTAGTGTGCTGCTGA 662  
Db 650 CTACAAAGTTGCTTGAAGTGTAGCTAGACACCAAGATCGCAACCC---TGCCTGTGCTGCGA 706  
Qy 663 CGCTGTTCTCAGCGCGGTCAAGCTGAGCTGGGGTTCCTTCAATTCAGCGCCCAAGGCCAT 722  
Db 707 CGCTCACCGCACCGGCCAAGGCAAGCTGGGGTTCCTTCAATTCAGCTCCCAAGGCCCT 766  
Qy 723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTGACGCAATCAAAAGTTCGTGTGAC 782  
Db 767 CTCGAGCTGAAAGAGCGAGCCACAAAGACTCTTGACGGGTGCTGCAAGTTCGTGTCAAC 826  
Qy 783 TGACGATGCTCTTTCGGCGTTCATCTGGAATCGGGCTCTCGCGTGGCTCGAAGAT 842  
Db 827 TGATGATGCTCTTTCGGCGTTCATCTGGAATCGGGCTCTCGCGTGGCTCGAAGAT 886  
Qy 843 CGATGCTCTGACCTTACCGAGTTCCTGCGGTGCTGTGATGCTCGACCGGCAATGGGT 902  
Db 887 GATGCTTCCACACTACTGATTCCTGCGCGCTGTGACATGCGGGGCCCCAATGGCGT 946  
Qy 903 CTCGAACAACTACCGAGCTTCTTCAAAACATGACTTACCACTGACCAATCGGCGA 962  
Db 947 ATCAAGCACAATACCGAGCTTCTTCAAAACATGACTTACCACTGACCAATCGGCGA 1006  
Qy 963 ATTCGCAAGGATGACTCGGCGACACGATCAGCTTCTGTCAGAACTCGACCCCGC 1022  
Db 1007 AATCGCAACGAAACCACTTGGGCGCAACGATCAGCTGCGCTCGAACTCAACAGTGA 1066  
Qy 1023 GAGCATGCGCCAGCGAAACAGAGGTCTCGGAGCTTACCTGCAACAAACCCCGACAAATC 1082  
Db 1067 TCGTTTGGCGAGACGAAACAGCTTGGGAGGTATCATGCTGCTGCTGACAAATGTC 1126  
Qy 1083 CAAAGCTATCCCTGACCGGTGATCGGACCCATCTACAGCGTATGCTGAGTTCTTGGGC 1142  
Db 1127 GAGCGTCTCCCTGACCGCGATCGGAATCGGTCAAGCAGCATCATGCTGAGTTCCTGGGC 1186  
Qy 1143 CAAAGTGGGACTTGGGATTAAGACTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAG 1202  
Db 1187 CAAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCCTGAGAGTGTGAG 1246  
Qy 1203 ACGGCCAATCTTTGAGCTTGTGAGAGTGTGATGATCTTTATGCCCAAGAGCTGATGG 1262  
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Db 1307 CGAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGA 1366  
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Db 1367 GAGTGGACCAAGTATGCGGAGTATTTGGGTAG 1400

RESULT 8  
US-10-074-279-10  
; Sequence 10, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 13737  
; TYPE: DNA  
; ORGANISM: Plasmid  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
US-10-074-279-10

Query Match 67.5%; Score 915.6; DB 4; Length 13737;  
Best Local Similarity 80.3%; Pred. No. 4.1e-283;  
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;  
Qy 3 GCCTTTCAGATACAGCTCGACACCTCGCGCAGCTACAGGCTCTCTTTCGATCTACAC 62  
Db 50 GTCCTTTCAGATACAGCTCGACATCATCGCGCAGCAACCGCTCTCTTTCGATCTACAC 109  
Qy 63 CCAATTCAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCAC 122  
Db 110 CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCCACTATCCCACTATCGTACGAC 169  
Qy 123 CTTTCAGCAGGCTTTAAGCGCTTCTCCGAGCGCTGCCATGGTTCGAGGCCAGGTCAA 182  
Db 170 CTTTCAGGAGGCGCTTAAACCGCTCTCTCAAACTTCCATGGTTCGCGGCCAGGTCAA 229  
Qy 183 AGCCGAGGCGCATTCAGCGGGAACACAGAACTTCTTATCGTCCCTTTTTCGAGACGT 242  
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Qy 243 TCCTCGTGTGTGAGTGAAGACCTCGCGATGATTCCTTCAGCGGCCCAACGATCGAGGTTAT 302  
Db 290 ACCCGCTCTGTGTGAGGAGACCTCGTGATGATTCCTTCAGCGGCCCAACGATCGAGGTT 349  
Qy 303 GAGAAAGCGGATACCCCTATTCGCGATGTTTTCGAGAAACATCATTCGCGGCCAAGGAAGAC 362  
Db 350 GAGAAAGCGGCTTTCCTTTCGAGATGTTTTCGAGAAACGCTCGTCTCCGAGGAGAC 409  
Qy 363 GTTACTATTGACCTGGTACTGTCGCGACGACCCCAAGCCCTGTAATTTCTATTGAGCT 422  
Db 410 ATTAGCTATCGGACCTTGGCAATGGCCCCAACGACCCGAGCTGTGTTGCTATTGAGCT 469  
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Db 470 CAACTTTCATCAGGGCGGACTCATCTCAACCGTCAACGGACCAACATGTTGCTATGAGCAT 529  
Qy 483 GGTAGGCCAAGATGCGGGTATCCGCTACTCTTCCAAAGCGGTGCGGTAAACGCCATTTCAC 542  
Db 530 GACAGGACAAAGATGCAATTTATTCGTCTTCTTCCAAAGCGGTGCGGCAACGAATCATTCAC 589  
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Db 590 CGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGCGGTAGTCTCTCTCTTCTTGAATA 649

603 CTATACGATTGGCCGAGGTAGATCATCAGATTGTCAAAGTGTAGTCTGGTGTGA 662  
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650 CTACAAAGTTGGTCTCTAGCTAGACACACAGATGCCAAAC--TGCAGCTGTCTGGCGA 706  
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663 CGCTGTTCTCAGCCGGTCAAGTCAAGTGGCGGTTCTTCAATTCAGCCCCCAAGGCCAT 722  
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707 CGCTCACCCGACCGGCCAAGCAAGCTGGGGGTTCTTTCACTTCACTCCCAAGGCCCT 766  
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723 GTACAGCTCAAGGATGTCTCAACAGACTTTGACGATCAACAAAGTTCTGTCTGAC 782  
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767 CTCGAGCTGAAGACGACGACCAAGACTCTTGACGCGTCTGCAAGTTTGTCTCAAC 826  
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783 TGAAGTGTCTTTGGCGGTTCTCTGGAATTCGGCTCTCGCGTCTCGAAGAAAT 842  
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827 TGAATGATGTCTTTGGCGGTTTATCTGGAATCAACCTCGCGGTAAGTCTCGCAAGAT 886  
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843 CGATGCTCTGACCTTACCGAGTTCTGCGGTTCTGTGTGATGCTCGACCGGCAATGGGT 902  
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887 GGATGTTTCAACCTACTGAATCTGCGCGTCTGACATGCGGGGCCAATGGGCT 946  
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903 CTCGAACAATACCCAGGCTTCTCAAAACATGACCTACCAACTCGACCATCGCGGA 962  
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947 ATCAAGCACAATACCCAGGCTTCTCAAAACATGACCTACCAACTCGACCATCGCGGA 1006  
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963 AATCGCAAGGATGATCTGGCGCAACAGCATCAAGCTTCTGTTCAAGAACTCGACCCCG 1022  
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1067 TCGTTTGGCAGAGCAACAACTTTGGCGAGTACATGATGCTGCGCTGCAAGATC 1126  
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1083 CAAGTATTCCTGAGCGGCTGATCGGACCACTTACAGGGTCTGCTGAGTTCTTGGG 1142  
|||  
1127 GAGCGTCTCCCTGACCGCGGATCGAATCGGTCAAGAGCATCATGCTGAGTTCTTGGG 1186  
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1143 CAAGTGGGACTCTGGGATTTACGATTTGGGCTCGGCTGAGTAAAGCCGAGATCTGTGAG 1202  
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1187 CAAGTGGGATCTGGGAGTATGACTTTGGGTTGGACTGGTAAAGCTGAGATGTGAG 1246  
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1203 ACGGCCAATCTTGAAGCTTCTGAGAGTCTGAGTCTTATGCTTATGCCCAAGAGCTGATGG 1262  
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1247 AAGACCTCGCTTTGAACCTTTGAGAGTTTGTATGATCTTTATGCCCAAGAGCTGATGG 1306  
|||  
1263 CGAGTTCTGCGCGGCTTCTCTGAGGATGAGGATATGACCGGATTTGAAGCGGATAA 1322  
|||  
1307 GGAGTTTACCGCGCTCAATTTCTGAGGGATGAGATATGAGAGACTAAAGCGGATGA 1366  
|||  
1323 GGAGTGACCAAGTATCGCAGTACGTTGGTTAG 1356  
|||  
1367 GGAGTGACCAAGTATCGCAGTATATTTGGGTAG 1400  
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## RESULT 9

US-09-538-414-7

; Sequence 7, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/09/538.414

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1425

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-09-538-414-7

Query Match 18.4%; Score 249.8; DB 3; Length 1425;

Best Local Similarity 51.9%; Pred. No. 9.1e-70;

Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGCTCCACACCCCTCGCCAGCTACCAAGGCTCTCTTTCGATCTACACCCCAATCAGTCTC 75  
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Db 124 ATCTACCGTGTACCAAGTCTCTTCTGCTCATGACCATATCGTAAATACCTTTAAACAAGGA 183  
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QY 1018 CCGCGAGCA-----TGGCGCAGCAACAAGAGTCTCGGACGTACCTTGCAACAAC 1071  
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QY 1192 GAGACTGTGAGAGCGGCAATCTTTGAGCCTTTGAGAGCTTTGATGACTTTTATGCCCCAAG 1251  
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QY 1252 AAGCCTGTATGGCGAGTTCTGTGCGGCGCTTTCTCTGAGGAGTATGAGCCGATTTG 1311  
DB 1321 TCCTCAGAGGTGAATGGTGTGCTCTTTGCTTTAGAGATAAAGATTGGGAGTGCCTG 1380  
QY 1312 AAGCGGATAAGGAGTGGACCAAGTATGC 1340  
DB 1381 AATGCGGATAAAGATGGCAATTTATGC 1409

## RESULT 10

US-10-074-279-7

; Sequence 7, Application US/10074279

; Patent No. 6646184

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/10/074,279

; CURRENT FILING DATE: 2002-02-12

; PRIOR APPLICATION NUMBER: US/09/538,414

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1425

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-10-074-279-7

Query Match 18.4%; Score 249.8; DB 4; Length 1425;  
Best Local Similarity 51.9%; Pred.No. 9.1e-70;  
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;  
QY 16 CAGCTCGACACCTCGGCGAGCTACAGGCTCCTTTCGATCTACACCCAAATCAGTCTC 75  
DB 64 CAACCTTGATATTTTGGGCAACAACCTTCGCTATACAAACTATACACTCAAAATATGCTCT 123  
QY 76 CTTACCCGCTCTCGATTCCTCAATATCCCACTATTGTACAGACCTTCGAGCAAGGT 135  
DB 124 ATCTACGTTGACAGATCCTCTGCTCATGACCATATGTAATACCTTAACAGAGA 193  
QY 136 CTTAAGCGCTTCTCGAAGCGTCCCATGGTGGCGAGGCGAGGTCAAAGCCGAGGCATT 195  
DB 184 CTTGAACATTGCTAAAAATTTCCAGTGGCTAGCAGGAAATGTCGTAATGAAGTGTCT 243  
QY 196 AGCGAGGAAACACAGAACTTCTTTATGCTCCCTTTTGGAGACGTTTCTCTGTTGTA 255

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QY 316 TACCTATGGCGATGTTTTCAGGAAACATCATCGCGCCAGGAGACGTT-----ACCT 369  
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QY 550 GAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTGAAAATCTATACG 609  
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QY 610 ATT---GGCCCGGAGGTAGATCATCATGATTTGTCAAAGCTGTATGCTGTGGTGAAGCT 666  
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QY 778 TCGACTGACGATGCTCTTTTCGGCGTTTCACTCGAAATCGGCTCTCGCGTCTCGAA 837  
DB 841 TCCACTGATGATATCGTCACTGCTTTCATCTGGAATCAGTTTCTCGAGCCGCTTATCT 900  
QY 838 AGAATCGATGGCTCTGCACTACCGAGTTCTGCGGCTGTGTTGATGCTCGACCGCAATG 897  
DB 901 CGACTTAAACCCAGAAAACGAAATCAAATTTAGGCGGTGCTGTGGATTTAGAAAACGGCTA 960  
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QY 1072 CCGCAAGTCCAAGCTATCCCTGACGGCTGTATGCGGACCCATCTACACGCGTCAATGCTG 1131  
DB 1141 CCGCAAGACTAAGGTTTCTATCTCAACCAATTTGATACTTTATCTGGAATTTAGGTC 1200  
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QY 1252 AAGCCTGTATGGGAGTTCTGTGGGCGCTTCTCTGAGGAGTATGAGGATGAGCCGATTCG 1311  
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QY      1312 AAGCGGATAAGGAGTGGACCAAGTATGC   1340
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DB      1381 AATGCGGATAAAGATGGACAATTATGC   1409

RESULT 11
US-09-103-840A-2
/ Sequence 2, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ APPLICANT: VENTER, John C.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ TITLE OF INVENTION: TUBERCULOSIS
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103,840A
/ CURRENT FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4403765
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ FEATURE:
/ OTHER INFORMATION: CDC 1551
/ OTHER INFORMATION: "n" bases at various positions throughout the sequence
/ OTHER INFORMATION: represent a, t, c or g

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Query Match          2.98; Score 39.8; DB 3; Length 4403765;
Best Local Similarity 49.8%; Pred. No. 2.6;
Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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Db      4219476  ACGCCACAGCATCCGCGAACTCGAAGATGGTCTGCGCCGGAACCTGCGGAGGAGCTCG 4219535

Qy      1076  ACAAGTCAAGTATCCCTGACGCTGATGGGACCCATCTACAGCGTCATCTGCTGAGTT 1135
Db      4219536  ACCGGCTTACCTGCCGTTCAACAGAGACGCGCTCGACGCCGAGTTGCGCATTC 4219595

Qy      1136  CTTGGGCCNAGGTGGGACTCTGG 1158
Db      4219596  CCCAGGCACAGCTGGTCGGCTGG 4219618

RESULT 12
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 04:49:05 ; Search time 4735 Seconds  
(without alignments)  
10435.539 Million cell updates/sec

Title: US-10-614-954-5  
Perfect score: 1356  
Sequence: 1 atggtttcaagatacagct.....atgcagctacgttggttag 1356

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	406	29.9	1055	4	BI947129
3	354.2	26.1	512	4	BI191800
4	351	25.9	508	4	BI191865
5	323.4	23.8	498	4	BI200717
C 6	317.6	23.4	499	4	BI191678
C 7	296.6	21.9	481	4	BI191864
8	278.4	20.5	514	4	BI192008
9	278	20.5	411	4	BI187781
C 10	273.4	20.2	448	4	BI201068
C 11	273	20.1	518	4	BI191997
C 12	268.4	19.8	457	4	BI187780
C 13	258	19.0	392	4	BI192452
C 14	254.8	18.8	423	4	BI192498
C 15	251.2	18.5	490	4	BI201353
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C 17	242.8	17.9	476	4	BI192381
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C 19	234.4	17.3	401	4	BI192451
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C 38	170.4	12.6	373	4	BI190682
C 39	170.4	12.6	376	4	BI189442
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C 43	169.4	12.5	360	4	BI187939
C 44	169.4	12.5	361	4	BI201147
C 45	169.4	12.5	379	4	BI189968

ALIGNMENTS

RESULT 1  
BI949616 899 bp mRNA linear EST 19-OCT-2001  
LOCUS HVSMEL0014017f Hordeum vulgare spike EST library HVCDNA0012  
DEFINITION (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone  
HVSMEL0014017f, mRNA sequence.  
ACCESSION BI949616  
VERSION BI949616.1 GI:16291032  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 899)  
AUTHORS Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R.,  
Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M.,  
Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W.,  
Oates, R. and Main, D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Fusarium infected Morex spike cDNA library  
Unpublished (2001)  
CONTACT: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 598  
Seq primer: AATTAACCTCCTACTAAAGG  
High quality sequence stop: 755.

JOURNAL COMMENT

Unpublished (2001)

Contact: Wing RA

Clemson University

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 598

Seq primer: AATTAACCTCCTACTAAAGG

High quality sequence stop: 755.

FEATURES

source

1..899

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Morex"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HVSMEL0014017f"

/lab\_host="TJCI21"

/clone\_lib="Hordeum vulgare spike EST library HVCDNA0012"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap

frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

## ORIGIN

Query Match 49.0%; Score 663.8; DB 4; Length 899;  
 Best Local Similarity 95.8%; Pred. No. 2.9e-184;  
 Matches 724; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCAGCTACAGGCTCTCTTCGATCTAC 60  
 DB 110 ATGGCTTTCAAGATACAGCTCGACACCTCGGCAGCTACAGGCTCTCTTCGATCTAC 169  
 QY 61 ACCCAATCATGCTCTCTACCCGCTCTGATCTCTCAATATCCCACTATTGTCAGC 120  
 DB 170 ACCCAATCATGCTCTCTACCCGCTCTGATCTCTCAATATCCCACTATTGTCAGC 229  
 QY 121 ACCTTCGCAAGGCTTCTAGCCGCTCTCCGAGCGCTCCATGCGTCCGAGCCAGGTC 180  
 DB 230 ACCTTCGCAAGGCTTCTAGCCGCTCTCCGAGCGCTCCATGCGTCCGAGCCAGGTC 289  
 QY 181 AAAGCCGAGGCTATTAGCGAGGAAACACAGGAACCTTCTTTATCGTCCTTTTGGAGC 240  
 DB 290 AAAGCCGAGGCTATTAGCGAGGAAACACAGGAACCTTCTTTATCGTCCTTTTGGAGC 349  
 QY 241 GTTCCTCGTTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCAGTCGAGGTT 300  
 DB 350 GTTCCTCGTTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCAGTCGAGGTT 409  
 QY 301 ATGAGAAAGCGGATACCTTATGGCGATGTTTGACGAGAACATCATCGCGCCAGGAAG 360  
 DB 410 ATGAGAAAGCGGATACCTTATGGCGATGTTTGACGAGAACATCATCGCGCCAGGAAG 469  
 QY 361 ACCTTACCTATTGACCTGTTGTTGTCCTCCGAGCCAGCCAAAGCTGTAATCTATTGCGAG 420  
 DB 470 ACCTTACCTATTGACCTGTTGTTGTCCTCCGAGCCAGCCAAAGCTGTAATCTATTGCGAG 529  
 QY 421 CTCAACTTCATCAAGGCGGACTCATCTCACTGTCAACGAGCAGCGTGTATGGAT 480  
 DB 530 CTCAACTTCATCAAGGCGGACTCATCTCACTGTCAACGAGCAGCGTGTATGGAT 589  
 QY 481 ATGCTAGGCCAAGATCGGTTGATCCGCTCTACTCTCCAAAGCGTCCGCTAACGCCCATTC 540  
 DB 590 ATGCTAGGCCAAGATCGGTTGATCCGCTCTACTCTCCAAAGCGTCCGCTAACGCCCATTC 649  
 QY 541 ACCGAAGAGGAATGACGGCCATGAACCTCATCGAAGCAGATAGTCTTACCTTGAA 600  
 DB 650 ACCGAAGAGGAATGACGGCCATGAACCTCATCGAAGCAGATAGTCTTACCTTGAA 708  
 QY 601 AACTATACGATTGCCCGGAGTAGATCATCAGATTGTCAAAGCTGATGTAGTGGTGGT 660  
 DB 709 AACTATACGATTGCCCGGAGTAGATCATCAGATTGTCAAAGCTGATGTAGTGGTGGT 768

QY 661 GACGCTGT-TCTCAGCGCGGTCACTGCAAGCTGGCGGCTTCTTCAATTCAGCCCCAGGC 719  
 DB 769 GTGACGCTGTCTCAGCGCGGTCACTGCAAGCTGGCGGCTTCTTCAATTCAGCCCCAGGC 827  
 QY 720 CATGTCAGAGCTCAAGGATGCTGCTACAGACTCT 755  
 DB 828 CATGTCANAGCTC-AGGATGCTGCTACAGAACTCT 862

## RESULT 2

BI947129

## LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTAACTCTCACTAAAGGG

High quality sequence start: 5

High quality sequence stop: 668

Location/Qualifiers

1..1055

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Morex"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HVSME10003N10f"

/tissue\_type="Spike"

/lab\_host="TJCI121"

/clone\_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library

preparation and sequence analysis see  
http://www.genome.clemson.edu/projects/barley. To order  
this clone see http://www.genome.clemson.edu/orders Also  
see Close TJ, Wing R, Kleinbols A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

ORIGIN

Query Match 29.9%; Score 406; DB 4; Length 1055;  
Best Local Similarity 79.4%; Pred. No. 3.9e-108; Indels 0; Gaps 0;  
Matches 481; Conservative 0; Mismatches 125; Indels 0; Gaps 0;  
QY 387 TCCGACGACCCAAAGCCTGTAATCTTATTCAGCTCAACTTCATCAAGGGCGACTCAT 446  
DB 1 TCCGACGACCCAAAGCCTGTAATCTTATTCAGCTCAACTTCATCAAGGGCGACTCAT 60  
QY 447 CCTCATCTGCAACGGACAGCAGCTGCTATGATATGCTAGGCCAAGATGCCGTGATCCG 506  
DB 61 GCTCACTGTCAACGGACAGCAGCTGCTATGATATGCTAGGCCAAGATGCCGTGATCCG 120  
QY 507 TCTACTCTCAAGCGCTGCGGTAAACGACCCATTACCGAAGAGGAAATGACGGCCATGAA 566  
DB 121 TCTACTCTCAAGCGCTGCGGTAAACGACCCATTACCGAAGAGGAAATGACGGCCATGAA 180  
QY 567 CTTGATTCGCAAGACGATATCTTCTTACCTTGAATACTATACGATTTGGCCCGAGGTAGA 626  
DB 181 CTTGATTCGCAAGACGATATCTTCTTACCTTGAATACTATACGATTTGGCCCGAGGTAGA 240  
QY 627 TCATCAGATTGCAAGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586  
DB 241 TCATCAGATTGCAAGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 687 AAGCTGGCGTCTTTCACATTCAGCCCAAGGCGATGTCAGAGCTCAAGATGCTCTCTAC 746  
DB 301 AACTGGGGTCTTTCACATTCAGCCCAAGGCGCTGTCAGAGCTCAAGATGCTCTCTAC 360  
QY 747 CAAGACTCTTACGCTCAACAAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806  
DB 361 CAAGACTCTTACGCTCAACAAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 807 CTGGAATCGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866  
DB 421 CTTGGAATCGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 867 CTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 926  
DB 481 GCAGCTGCTATTAACGCTACCGGGCAGAGTGTACCAAGCAATCCCAACCTTAGCC 540  
QY 927 TCAAAACATGACCTTACCAACTCGACCATCGCGGAAATCGCCAAACGAGTCACTCGGCG 986  
DB 541 TCGTGAACACGCTTTCCAAACGTAACCGCGGCAACGCGCATCGTGTCTCGCGGGA 600  
QY 987 AACAGC 992  
DB 601 ACCAGC 606

RESULT 3

BI191800 512 bp mRNA linear EST 10-JUL-2001  
LOCUS 121115.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
DEFINITION library Fusarium sporotrichioides cDNA clone 121115 5', mRNA  
sequence.  
BI191800 1 GI:14665479  
VERSION 1  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides  
ORGANISM Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
REFERENCE 1 (bases 1 to 512)  
AUTHORS Ren.Q., Tag.A., Peglow.A., Lai.H., Kupfer.C., Peterson.A.,

TITLE  
JOURNAL  
COMMENT

Beremand, M. and Roe, B.  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Other ESTs: 121115.f1  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
871 8e-94 gi|4378882|gb|AAD197 (AF127176)  
trichothecene3-O-acetyltransfer  
Seq primer: T3  
High quality sequence stop: 476.

FEATURES  
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/organism="Fusarium sporotrichioides"  
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/strain="Tri 10"  
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cDNA library"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBluescript; 3' end of cDNA cloned into XhoI site of  
pBluescript"

ORIGIN

Query Match 26.1%; Score 354.2; DB 4; Length 512;  
Best Local Similarity 82.2%; Pred. No. 6.3e-93;  
Matches 407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 3 GGCCTTCAAGATACAGCTCGACACCTCGGCGAGCTACCGGCTCTCTTGCATCTACAC 62  
DB 16 GTCTTTGACATAGAGCTCGACATCATCGCGAGCAACCGCTCTTCTTCACTACAC 75  
QY 63 CCAATTCAGTCTCTTACCCGCTCTGATCTCTCAATATCCACATATGTCAGCAC 122  
DB 76 CCAGATCAGTCTGCTTACCCGCTCTGATCTCTCCAGTATCCACCATGTCAGCAC 135  
QY 123 CTTTCAGCAAGGCTTCTTAAGCGCTTCTCCAAAGCGCTCCATCGGTCGAGGCGAGTCAA 182  
DB 136 CTTTCAGCAAGGCTTCTTAAGCGCTTCTCCAAAGCGCTCCATCGGTCGAGGCGAGTCAA 195  
QY 183 AGCCGAGGCGATTCAGCGAGGAAACACAGGAATCTCTCTTATCGTCCCTTTTGGAGAGCT 242  
DB 196 GACCGAGGCGATTCAGCGAGGAAACACAGGAATCTCTCAAGATCATTTCCATATGAGGAGAC 255  
QY 243 TCCTCGTGTGTAGTGAAGAGCTCGGATGATCTTTCAGCGCCACCATCGAGGGTAT 302  
DB 256 ACCCGGTCTTGTGGTGAAGAGCTTCGATGATCTTCCAGCGCCAAACATCGAGGGT 315  
QY 303 GAGAAAGCGCGATACCCCTATGCGATGTTTCAGAGAAACATCATCGCCCAAGGAAGAC 362  
DB 316 GAGAAAGCGGGTTCCTCTTAGAGATGTTTCAGAGAAACGTCGTCCTCCGAGGAGAC 375  
QY 363 GTTACTTATGACCTGTGTACTGTTGTCGAGCCCAAGAGCTGTAACTTATTCAGCT 422  
DB 376 ATTAGTATCGGACCTTGGCAATGGCCCAACGACCGGAGCTGTGTGTTATTCAGCT 435  
QY 423 CAACCTCATCAGGCGGAGCTCATCTCACTGTCAACGAGCAGCAGGTCGTATGATAT 482  
DB 436 CAACCTCATCAGGCGGAGCTCATCTCACTGTCAACGAGCAGCAGGTCGTATGATAT 482  
QY 483 GGTAGGCCAAGATGC 497  
DB 496 GACAGCAAGATGC 510

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RESULT 4
BI191865      508 bp mRNA linear EST 10-JUL-2001
LOCUS        13b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION   library Fusarium sporotrichioides cDNA clone 13b10fs 5', mRNA
sequence.
BI191865     1 GI:14665544
EST.
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 508)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other_ESTs: 13b10fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
857 3e-92 gi|4378882|gb|AAD197 (AF127176)
trichothecenes-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 450.
Location/Qualifiers
1..508
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/strain="Tri 10"
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cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

FEATURES
Source
Query Match 25.9%; Score 351; DB 4; Length 508;
Best Local Similarity 81.8%; Pred. No. 5.6e-92;
Matches 405; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 3 GGCTTTCAAGATACAGCTCGACACCTCGCCAGCTACAGGCTCTCTTCGATCTACAC 62
Db 13 GTCTTTTGACATAGAGCTCGACATCATCGGCAGCAACCCGCTCTCTTCAATCTACAC 72

Qy 63 CCAATCAGTCTCTCTACCCCGCTCTGATTCCTCTCAATATCCCACTATTCGAGCAC 122
Db 73 CCAGATCAGTCTCTTTACCCCGCTCTGATTCCTCCAGTATCCCACTATTCGAGCAC 132

Qy 123 CTTGAGCAAGGCTTTAAGCGCTTCTCGAAGCGCTCCATGGTCCAGGCCAGGTCAA 182
Db 133 CTTTGAGGAGGCTTAAACCGCTCTGTCAACCTTCCCATGGTCCGGGCCAGGTCAA 192

Qy 183 AGCCGAGGCAATAGCAGGGAACACAGGAACCTTCCTTTATCTCTCTTTGAGGACGT 242
Db 193 GACCGAGGCAATAGCAGGAGGAGACACAGGAACCTTCAGATCATTCATATGAGGAGAC 252

Qy 243 TCCTCGTGTTCGTGAAAGACCTTCGCGATGATCTTCACGCGCCACGATCGAGGTAT 302
Db 253 ACCCGCTCTTCGTGAAAGACCTTCGCGATGATCTTCACGCGCCACGATCGAGGTAT 312

Qy 303 GAGAAAGCGGATACCTTCATGGCGATGTTTGACGAGAACATCATCGCGCCAGGAGAC 362

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Db 313 GAGAAAGCGCGGTTTCCCTTAGAGATGTTTGACGAGAACGTCTGCTCCGAGGAAGAC 372
Qy 363 GTTACCTATTGGACCTGCTACTGTCGCCGACGACCCAAAGCCTGTATTTCTATTGCAGCT 422
Db 373 ATTAGCTATCGGACCTGGCAATGCCCCAACAGACCCCGAGCCTGTGTGCTATTGCAGCT 432
Qy 423 CAATCTTCATCAAGGCGGACTCATCTCTCACTGTCAACGAGACAGACCGTGTGTATGATAT 482
Db 433 CAATCTTCATTAAGGCGGACTCATCTCTCACTGTCAACGAGACAGACCGTGTGTATGATAT 492
Qy 483 GGTAGGCCAAGATCC 497
Db 493 GACAGGACCAAGATCC 507

RESULT 5
BI200717     498 bp mRNA linear EST 10-JUL-2001
LOCUS        ole06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION   library Fusarium sporotrichioides cDNA clone ole06fs 5', mRNA
sequence.
BI200717     1 GI:14666689
EST.
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 498)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
743 8e-79 gi|4378882|gb|AAD197 (AF127176)
trichothecenes-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.
Location/Qualifiers
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/db_xref="taxon:5514"
/clone="ole06fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

FEATURES
Source
Query Match 23.8%; Score 323.4; DB 4; Length 498;
Best Local Similarity 79.2%; Pred. No. 7.8e-84;
Matches 397; Conservative 0; Mismatches 101; Indels 3; Gaps 1;

Qy 443 TCATCTCTACTGTCAACGAGCAGCAGCGTGTCTATGATATGATAGCCAAAGATCGGTGA 502
Db 1 TCATCTCTACCGTCAACGAGCAGCAGCGTGTCTATGATATGATAGCCAAAGATCGGTGA 60

Qy 503 TCCTGTCTACTTCCAAAGGCGTCCGTAACGACCCATTTCACCGAGAGGAAATGACGGCCA 562
Db 61 TTCTGTCTCTCTCCAAAGGCGTCCGTAACGACCCATTTCACCGAGAGGAAATCTCGGCCA 120

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/mol type="mRNA"

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/strain="Tri 10"
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/db xref="taxon:5514"
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/clone="13b10fs"
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/clone-1301015
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cdna library"

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CDNA library  
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:

XhoI: 5' end of cDNA cloned into EcoRI site of

pBluescript: 3' end of cDNA cloned into XhoI site of

"Fairbanks" b7c b7d b7e b7f b7g b7h b7i b7j b7k b7l b7m b7n b7o b7p b7q b7r b7s b7t b7u b7v b7w b7x b7y b7z

## ORIGIN

Query Match	21.98;	Score 296.6;	DB 4;	Length 481;
Best Local Similarity	80.5%;	Pred. No. 6.3e-76;		
Matches 347;	Conservative 0;	Mismatches 84;	Indels 0;	Gaps 0;
Qy	926	TTCAAAACATGACCTACCAACATCGACCATCGCGAAATCGCAACAGAGTCACTCGCG	985	
Db	481	TTCAAAACATGACCTACCAACATCGACCGTGGCGAAATCGCCAGAACCACTTGGCG	422	
Qy	986	CAACAGCATCACGCCCTTCGGTTCAGAACTCGACCCCGGAGCATGCGCCAGCAACAAG	1045	
Db	421	CAACAGCATCACGCCCTCGGTTCGAACTCAACAGTATCGTTTCGGCAGACGAACACAG	362	
Qy	1046	GTCTCGCGAGGTACTCTGCACAAACACCCGACAAAGTCCAAGTATCCCTGACGGCTGATG	1105	
Db	361	CTTTGGCGACGTACATGATGGCTGCTGCACAAAGTCAGCGTCTCCTGACCCCGATG	302	
Qy	1106	CGGACCATCTACAGCGTCAATGCTGAGTCTCTTGGCCCAAGTGGGACTCTGGGATTCG	1165	
Db	301	CGAATCGTCAAGCAGCATCATGCTGAGTTCCTGGCCAAAGTGGGATGCTGGGAGTATG	242	
Qy	1166	ACTTTGGGCTCGGACTCGGTTAAGCCCGAGACTGTGAGACGCCCAATCTTTGAGCGCTGTG	1225	
Db	241	ACTTTGGGTTTGACTCGGTTAAGCCTGAGAGTGTGAGNAGACCTCGCTTTTGAAACCTTTG	182	
Qy	1226	AGACCTTGATGACTTTTATGCCCAAGAGCCTGATGGGAGTTCGTGTCGGCGCTTTCTC	1285	
Db	181	AGA GTTTGATGACTTTTATGCCCAAGAGCCTGATGGGAGTTTTCACGCGCTCCATTTCTT	122	
Qy	1286	TGCGGATGAGGATATGACCCGATTTGAAGGCGGATTAAGGAGTGGACCAAGTATGCGAGT	1345	
Db	121	TGAGGATGAGCATATGAGAGACTTAAGGCGGATGAGGAGTGGACCAAGTACGCAAGT	62	
Qy	1346	ACGTTGGTTAG	1356	
Db	61	ATATTGGGTAG	51	

RESULT 8  
BI192008  
LOCUS  
DEFINITION  
BI192008 514 bp mRNA linear EST 10-JUL-2001  
l4c09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone l4c09fs 5', mRNA  
sequence.

ORGANISM

TITLE Analysis of a Fusarium sporotrichioides EST database  
JOURNAL Unpublished (2001)  
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912

Fax: 405 325 7762  
Email: [bree@ou.edu](mailto:bree@ou.edu)  
Contact Dr. Marian Beremand regarding clone availability. Included  
is the best homology from a blastx search of Genbank nr 04-09-01  
730 3e-77 g1|4378882|gb|AAU197 (AF127176)  
trichothecene3-O-acetyltransfer  
seq primer: T3  
High quality sequence stop: 476.

## FEATURES

source

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/mol type="mRNA"

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/db xref="taxon:5514"
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/clone="14c09fs"
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CDNA Library"

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XhoI: 5' end of cDNA cloned into EcoRV

3' end of cDNA cloned in Bluescript: 3' end of cDNA cloned in

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pbValuescript; 3 emu of data classes 1
nValuescript"
```

## ORIGIN

Query Match	20.5%;	Score	278.4;	DB	4;	Length	514;
Best Local Similarity	81.0%;	Pred. No.	1.5e-70;				
Matches	324;	Conservative	0;	Mismatches	76;	Indels	0;
Gaps	0;						

  

QY	3	GGCTTTCAAGATACAGCTCGACACCCCTCGCGCAGCTACCGAGGCTCCTCTTCGATCTACAC	62
DB	115	GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCTCTTCTTCAATCTACAC	174
QY	63	CCAAATCAGTCTCCTCTACCCCGGCTCTGATTCCTCTCAATATCCCACTATTGTCCAGCAC	122
DB	175	CCAGATCAGTCTCGTTTACCCCGTCTGTGATCCCTCCAGTATCCCACTCGTCGACGAC	234
QY	123	CTTCGACACAGGCTTTAAGCGCTTCTCCGAGCGCGTCCCATGGGTGCGCAGGCCAAGGTCAA	182
DB	235	CCTTTGAGGAAGGCGCTAAAGCGCTCTCTCAAACTTCCCATGGGTGCGGGCCAGGTCNA	294
QY	183	AGCCGAGGGCATTAACGAGGGAAACACAGGAACCTTCCTTTATCGTCCTTTTGGAGGAGCT	242
DB	295	GACCGAGGGCATCAGCGGAGGAAACACAGGAACCTTCCAAAGATCATTCATATGAGGAGAC	354
QY	243	TCCTCGTGTGTGATGTGAAAGACCTCCGGGATGATCCTTCAGCGGCCACGATCGAGGGTAT	302
DB	355	ACCCCGCTCTGTGTGTGAAGACCTCCCGTGTGATTCCTTCAGCGGCCAACGATCGAGGGGTT	414
QY	303	GAGAAAGCGGGATACCTTATGGCGGATGTTTGGACGAGAAACATCATCGCGCCCAAGGAAGAC	362
DB	415	GAGAAAGCGGGTTTCCCTTTAGAGATGTTTGAAGAGAACGTCGTCGCTCCGAGGAAGAC	474
QY	363	GTTTACCTATTGGACCTGGTACTGTGTCGACGACGCCAACG	402
DB	475	ATTAGCTATCGGACTGGCAATGGCCCAAGCCGAGG	514

RESULT 9			
BI187781			
LOCUS	411 bp	linear	EST 10-JUL-2001
DEFINITION	BI187781	mRNA	
	b2404fs.r1	Fusarium sporotrichoides Tri 10 overexpressed cDNA	
	library	Fusarium sporotrichoides cDNA clone b2d04fs 5', mRNA	
		sequence.	

ACCESSION BI187781.  
VERSION BI187781.1 GI:14661460  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides  
ORGANISM Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium.  
1 (bases 1 to 411)  
REN, Q., TAG, A., PEPILOW, A., LAI, H., KUPFER, C., PETERSON, A.,  
BEREMAND, M. and ROE, B.  
REFERENCE Analysis of a Fusarium sporotrichioides EST database  
AUTHORS TITLE



JOURNAL Unpublished (2001)  
COMMENT Other ESTs: b20404fs.f1  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
591 4e-61 gi|4378882|gb|AAD197 (AF127176)  
trichothecenes3-O-acetyltransfer  
Seq primer: T3  
High quality sequence stop: 307.  
Location/Qualifiers  
1. .411  
/organism="Fusarium sporotrichioides"  
/mol\_type="mRNA"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
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cDNA library"  
/notes="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBlueScript; 3' end of cDNA cloned into XhoI site of  
pBlueScript"

ORGANISM Fusarium sporotrichioides  
REFERENCE 1 (bases 1 to 448)  
AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,  
Beremand, M. and Roe, B.  
TITLE Analysis of a Fusarium sporotrichioides EST database  
JOURNAL Unpublished (2001)  
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
594 4e-73 gi|4378882|gb|AAD197 (AF127176)  
trichothecenes3-O-acetyltransfer  
Seq primer: M13-20  
High quality sequence stop: 303.  
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/clone="o4c12fs"  
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cDNA library"  
/notes="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBlueScript; 3' end of cDNA cloned into XhoI site of  
pBlueScript"

ORIGIN  
Query Match 20.5%; Score 278; DB 4; Length 411;  
Best Local Similarity 81.2%; Pred. No. 1.9e-70;  
Matches 336; Conservative 0; Mismatches 75; Indels 3; Gaps 1;  
QY 401 AGCCTGTAATCTTATTCGAGCTCAACTTCAATCAAGGCGGAGCTCATCTCCTCAACG 460  
Db 1 AGCCTGTGTGCTATTCGAGCTCAACTTCAATCAAGGCGGAGCTCATCTCCTCAACG 60  
QY 461 GACAGCAGCGTGCTATGGATATCGTATAGGCCAAGATCGGTGATCGCTCTACTCTCCAAG 520  
Db 61 GACAACATGCTGTATGGATATGACAGGACAGATGCAATATTCGTCTCTCCTCAAG 120  
QY 521 CGTCCGTAACGACCAATTCACCGAAGAGAGAAATGACGGCCATGAACCTCGATCGCAAGA 580  
Db 121 CGTCCGCAACGAATCATTCACCGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGA 180  
QY 581 CGATAGTCTCTTACCTTGAACACTATACGATTCGCCCGGAGGTAGATCATCAGATTGTCA 640  
Db 181 CGGTAGTCTCTCTTGAACACTATACGATTCGCCCGGAGGTAGATCATCAGATTGTCA 240  
QY 641 AAGCTGATGTAGTGTGTGTGAGCTGTTCTCACGCCGGTCACTGCAAGCTGGGCGTTCT 700  
Db 241 AACC--TGGCGCTGTGGGAGCGCTCCACCGCAGCGGCAGGCAGCTGGGCGTTCT 297  
QY 701 TCATCTACGCCCAAGGCATGTCTAGAGTCAAGGATGTCTACCAAGACTCTTTGACG 760  
Db 298 TTTCAITCTACTCCCAAGGCCCTCTCGAGCTGAAGACGAGCCACCAAGACTCTTTGACG 357  
QY 761 CATCAACAAGTTCGTGTGACGATGATGCTCTTTTCGGCGTTTCATCTGGAAT 814  
Db 358 CGTCGTCGAAGTTGTGTCAACTGATGATGCTCTTTTCGGCGTTTCATCTGGAAT 411

RESULT 10  
BI201068/c 448 bp mRNA linear EST 10-JUL-2001  
LOCUS o4c12fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
DEFINITION library Fusarium sporotrichioides cDNA clone o4c12fs 3', mRNA  
sequence.  
ACCESSION BI201068  
VERSION BI201068.1 GI:14667040  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides

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Db 448 CGTGGCGCAATCGCCACGAAACCACTTGGCGCAACAGCATCAGCGCTTCGTTTCAGAACT 389  
QY 1014 CGACCCCGCGAGATCGCGCCAGCAACAAGAGTCTCTCGGACGTACTTCGACAAACCCC 1073  
Db 388 CAACAGTGATCGTTGGCGAGAGACACAAGCTTTGGCGAGCTACATGATGCGCTGCC 329  
QY 1074 CGACAAGTCAACGATTCCTGACGGCTGATCGGACCCATCTACAGCGTCTATGCTGAG 1133  
Db 328 TGACAAGTCGAGCGTCTCCCTGACCGCCGATGCGAATCCGTCAAGCAGCATCATGCTGAG 269  
QY 1134 TTCTTGGGCAAGTGGGAGCTCGGATTTACGACTTTGGCTCGGACTGGTAAGCCGA 1193  
Db 268 TTCTTGGGCAAGTGGGAGCTCGGATTTACGACTTTGGCTCGGACTGGTAAGCCGA 209  
QY 1194 GACTGTGAGACGCGCAATCTTTGAGCTCTGTGAGAGCTTTGATGTACTTTATGCCAAGA 1253  
Db 208 GAGTGTGAGAACCTCGCTTTGAACCTTTTGAGAGTTTGTATGTACTTTATGCCAAGA 149  
QY 1254 GCTGATGCGGAGTTCTGTGCGCGCTTCTCTGAGGAGTATGAGGATATGACCGATGAA 1313  
Db 148 GCCTGATGCGGAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAA 89  
QY 1314 GCGGATAGGAGTGGACCAAGTATGCGGAGTACGTTGGTTAG 1356  
Db 88 GCGGATAGGAGTGGACCAAGTATGCGGAGTATGAGGATATTTGGGTAG 46

RESULT 11  
BI191997 518 bp mRNA linear EST 10-JUL-2001  
LOCUS BI191997  
DEFINITION 14b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA

library Fusarium sporotrichioides cDNA clone 14b10fs 5', mRNA  
sequence.  
BI191997  
BI191997.1 GI:14665676  
EST.  
Fusarium sporotrichioides  
Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.  
1 (bases 1 to 518)  
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,  
Beremand, M. and Roe, B.  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
712 3e-75 gi|4378882|gb|AAD197 (AF127176)  
trichothecene3-O-acetyltransfer  
Seq primer: T3  
High quality sequence stop: 484.  
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/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBluescript; 3' end of cDNA cloned into XhoI site of  
pBluescript"  
ORIGIN  
Query Match 20.1%; Score 273; DB 4; Length 518;  
Best Local Similarity 80.9%; Pred. No. 6e-69;  
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Db 186 CCAGATCAGTCTCTTTACCCCGTCTCTGATCTCTCCAGTATCCCACTATCTCAGCAC 245  
Qy 123 CTTCGAGCAAGGCTTTAAGCGCTTCTCCGAAGCGGTCCCAATGGGTTCGAGCCAGGTCAA 182  
Db 246 CTTTGAGGAAGGCTTAAAGCGCTCTCTCAAGCGTCTCCCATGGGTTCGCGGCCAGGTCAA 305  
Qy 183 AGCCGAGGCGATTAGCGGGAACACAGGAACTTCTTTATCTGTCCTCTTTTGGAGAGCT 242  
Db 306 GACCGAGGCGATCAGCGGAAGAAACACAGGAATCTTCCAAATGATTCATATAGGAGAC 365  
Qy 243 TCCTCGTGTCTAGTGAAGACCTCCGCGATGATCTTTCAGCGCCCAACGATCGAGGGTAT 302  
Db 366 ACCCGTCTTGTGTGAAGACCTCCGATGATCTCTCAGCGCCCAACGATCGAGGGT 425  
Qy 303 GAGAAAGCGGGATACCCCTATGGCGATGTTTGAAGAGACATCATCGGCCAAGGAGAC 362  
Db 426 GAGAAAGCGGGTTTCCCTTAGAGATGTTTGAAGAGACATCGTCTCGTCCGAGGAAGAC 485  
Qy 363 GTTACCTATTGAGCTGTGCTGTTGTCGCGAGA 395  
Db 486 ATTAGTATCGGACCTGCGCAATGGCCCCAACA 518

RESULT 12  
BI187780/c  
LOCUS  
DEFINITION  
457 bp mRNA linear EST 10-JUL-2001  
b2d04fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA  
sequence.  
BI187780  
BI187780.1 GI:14661459  
EST.  
Fusarium sporotrichioides  
Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.  
1 (bases 1 to 457)  
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,  
Beremand, M. and Roe, B.  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Other ESTs: b2d04fs.r1  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
655 5e-70 gi|4378882|gb|AAD197 (AF127176)  
trichothecene3-O-acetyltransfer  
Seq primer: M13-20  
High quality sequence stop: 257.  
Location/Qualifiers  
1. 457  
/organism="Fusarium sporotrichioides"  
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cDNA library"  
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XhoI; 5' end of cDNA cloned into EcoRI site of  
pBluescript; 3' end of cDNA cloned into XhoI site of  
pBluescript"  
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Query Match 19.8%; Score 268.4; DB 4; Length 457;  
Best Local Similarity 80.0%; Pred. No. 1.3e-67;  
Matches 328; Conservative 0; Mismatches 81; Indels 1; Gaps 1;  
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Db 454 ACTCGACCTCGCGAATTCGCCAATCGCAGCAACGCAACGCAACGCAACGCAACGCA 396  
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Db 395 CGAACTCAACAGTATCGTCTTTCGCGAGCAAGCAACGCTTTGGCGAGTACATGCGATG 336  
Qy 1067 ACNACCCGACAGTCCACAGTATCCTCGCGGTGATGCGGACCCATCTACAGCGTCA 1126  
Db 335 GCTCTGCTGACAGTGCAGCGTCTCTCTGACCGCGATCGGATCGGATCGGATCGGATCA 276  
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Db 275 TGCTGAGTCTTGGGCCAAGGTGGGATGCTGGAGTATGACTTTGGGTTTGGACTGGGTA 216  
Qy 1187 AGCCGAGACTGTGACACGCGCAATCTTTGACGCTTTCGAGAGCTTGATGTTACTTATGC 1246  
Db 215 AGCCTGAGAGTGTGAGAAACCTCGCTTTTGAACCTTTTGAGAGTTTGTATGTTATGTC 156



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QY 1247 CCAGAGCCTGATGCGGAGTTCTGTGCGCGCTTCTCTGAGGATGAGGATATGGACC 1306
DB 155 CCAAGAGCCTGATGCGGAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGGAGA 96
QY 1307 GATTGAAGCGGATAGGAGTACCAAGTATGCGCAGTACGTTGGTTAG 1356
DB 95 GACTAAAGCGGATGAGGATGAGCAAAAGTACGCAAAAGTATATTTGGTTAG 46

RESULT 13
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DEFINITION library Fusarium sporotrichioides cDNA clone m4b09fs 5', mRNA
sequence.
ACCESSION BI192452
VERSION BI192452.1 GI:14666131
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE 1 (bases 1 to 392)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: m4b09fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Is the best homolog from a blastx search of Genbank nr 04-09-01
557 3e-57 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 361.
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cDNA library"
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XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

ORIGIN
Query Match 19.0%; Score 258; DB 4; Length 392;
Best Local Similarity 80.2%; Pred. No. 1.5e-64;
Matches 316; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

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QY 407 TAATTTCTATGAGCTCACTTATCAAGGCGGACTCATCTCACTGTCAAGGACAGC 466
DB 61 TGTGTGTTATGCACTCACTTATTAAGGCGGACTCATTTCTCAACGCAAGCAAC 120

QY 467 ACCGTGCTATGGATATGGTAGGCAAGATGCGGTGATCCGTTACTCTCAAGCGCTGCC 526
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QY 527 GTAAACGACCCATTACCGAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAG 586

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DB 181 GCAACGAATTATTCACCGAGGAGAAATCTGCGCCATGAACCTCGATCGCAAGACGGTAG 240
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DB 241 TCCTCTCTCTTGAAACTACAAAGTTGGTCTGAGCTATACCACCATGATCGCCAAACC-- 298
QY 647 ATGTAGCTGCTGCTGACGCTGTTCTCACCCCGTCTAGTCAAGCTGGGCGTTCTTCACAT 706
DB 299 -TGGCCTCTGCTGGCGACGCTCCACCGCACCGCCCAAGCAAGCTGGGCGTTCTTTTCAT 357
QY 707 TCAGCCCCCAAGCCATGTCAGAGCTCAAGGATGC 740
DB 358 TCACTCCCAAGGCCCTCTCGGAGCTGAAAGACGC 391

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DEFINITION library Fusarium sporotrichioides cDNA clone m4f10fs 3', mRNA
sequence.
ACCESSION BI192498
VERSION BI192498.1 GI:14666177
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE 1 (bases 1 to 423)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: m4f10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Is the best homolog from a blastx search of Genbank nr 04-09-01
652 3e-68 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 290.
Location/Qualifiers
1. .423
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cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
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pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"

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Matches 301; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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DB 423 CTTGGCGCAACAGCATCACGCTTCTGCGCTCGGAACCTCAACAGTATCGTTTGGCAGACGA 364
QY 1039 ACAAGAGTCTCGGAGCTACCTGCAACAAACCCCGCAAGTCCACGATTCCTTGACC 1098

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 21:19:40 ; Search time 731 Seconds  
(without alignments)  
9737.640 Million cell updates/sec

Title: US-10-614-954-5  
Perfect score: 1356  
Sequence: 1 atggtttcaagatacagct.....atgcgcagtaoigtggttag 1356

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

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- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	915.6	67.5	1403	3	AA54206 Sequence
5	915.6	67.5	12949	3	AA54213 Transform
6	915.6	67.5	13737	3	AA54212 Transform
7	249.8	18.4	1425	3	AA54210 Sequence
8	146.2	10.8	695	3	AA54210 Sequence
9	116.2	8.6	482	8	AB254817
10	50.4	3.7	2000	8	ADA71938 Rice gene
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12	39.8	2.9	663	12	AD181367 M. tuberc
13	39.8	2.9	110000	4	AA199682_42
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15	36.4	2.7	1605	2	AAT37310 Aromatic
16	35.8	2.6	2463	10	ADB68880
17	35.6	2.6	1459	6	ABQ33693 Oligonuc
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C	26	35.6	2.6	110000	12	ADN47960_08	Continuation (9 of
C	27	35.4	2.6	4526	10	ADB52532_08	Abd52532 Primary r
C	28	35.4	2.6	349980	5	AAH41233	AAH41233 Pyrococcus
C	29	34.8	2.6	2064	10	ADF44504	Adf44504 Mouse kinase
C	30	34.8	2.6	2753	10	ADF44505	Adf44505 Mouse kinase
C	31	34.8	2.6	3487	10	ADF44491	Adf44491 Mouse kinase
C	32	34.6	2.6	427	12	ADI42469	Adi42469 Plant transcript
C	33	34.6	2.6	1581	12	ADL81791	Adl81791 P. aeruginosa
C	34	34.6	2.6	84830	12	ADL81732	Adl81732 P. aeruginosa
C	35	34.2	2.5	720	11	ABD17428	Abd17428 Pseudomonas
C	36	34.2	2.5	1074	11	ABD17964	Abd17964 Pseudomonas
C	37	34.2	2.5	1497	10	ADF75240	Adf75240 Thale cress
C	38	34.2	2.5	2721	11	ABD17540	Abd17540 Pseudomonas
C	39	34.2	2.5	7234	5	AA574818	AA574818 DNA encoding
C	40	34	2.5	369	10	ABZ40050	ABZ40050 N. gonorrhoeae
C	41	34	2.5	1584	8	ACA39205	ACA39205 Prokaryotic
C	42	34	2.5	1713	12	ADL03328	Adl03328 DNA encoding
C	43	34	2.5	3115	6	ABQ43653	Abq43653 Oligonucleotide
C	44	34	2.5	3115	6	ABQ43652	Abq43652 Oligonucleotide
C	45	34	2.5	269223	4	AAF28554	AAF28554 Genomic fragment

ALIGNMENTS

RESULT 1  
AA54209  
ID AAA54209 standard; DNA; 1356 BP.

XX AA54209;

DT 15-SEP-2003 (revised)  
DT 26-FEB-2001 (first entry)

XX Sequence encoding trichothecene resistance polypeptide.

XX Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;  
wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
ds.

XX Gibberella zeae.

XX Key Location/Qualifiers  
FT CDS 1..1356  
FT /tag= a  
FT /product= "Trichothecene resistance polypeptide"

XX WO200060061-A2.

XX PD 12-OCT-2000.

XX PF 29-MAR-2000; 2000WO-EP002769.

XX PR 31-MAR-1999; 99US-00282995.

XX PR 11-FEB-2000; 2000US-00502852.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hohn TM, Peters C, Salmerton JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.

XX P-PSDB; AAB03935.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley

XX or rice plant, comprises heterologous polynucleotide encoding gene

XX product expressed in cell, having trichothecene resistance activity.

XX Claim 8; Page 48-49; 62pp; English.

XX A heterologous gene encoding a gene product which confers trichothecene  
CC resistance can be used to transform plant cells to make them resistant to  
CC fungal infection. The transformation method is useful for preventing  
CC mycotoxin contamination of a plant, particularly a crop plant such as  
CC wheat, maize, barley or rice, and for reducing and/or preventing the  
CC growth of a fungus of the genus *Fusarium* that produces a trichothecene,  
CC preferably comprising a C-3 hydroxyl group, by growing transformed crop  
CC plants in an area which is moderate to severe fungal infestation.  
CC (Updated on 15-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;

Query Match 100.0%; Score 1356; DB 3; Length 1356;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCGAGCTACCGAGGCTCTTTTCGATCTAC 60  
QY 61 ACCCAATCAGTCTCTTACCCGCTCTGATCTCTCTCAATATCCCACTATTCTCAGC 120  
DB 61 ACCCAATCAGTCTCTTACCCGCTCTGATCTCTCTCAATATCCCACTATTCTCAGC 120  
QY 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTCCGAGCCAGGTC 180  
DB 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTCCGAGCCAGGTC 180  
QY 181 AAAGCCGAGGGCATTTAGCGAGGGAACAAGGAACTTCTTTATGTCCTTTTTCAGGAC 240  
DB 181 AAAGCCGAGGGCATTTAGCGAGGGAACAAGGAACTTCTTTATGTCCTTTTTCAGGAC 240  
QY 241 GTTCTCTGTTTGTAGTGAAGACCTCCGCGATGCTCTTCGCGCCACGATCAGGGGT 300  
DB 241 GTTCTCTGTTTGTAGTGAAGACCTCCGCGATGCTCTTCGCGCCACGATCAGGGGT 300  
QY 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTTCAGAGAAACATCATCGCGCCAGGAAG 360  
DB 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTTCAGAGAAACATCATCGCGCCAGGAAG 360  
QY 361 ACGTTACTTATGGAACCTGTTGTCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 420  
DB 361 ACGTTACTTATGGAACCTGTTGTCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 420  
QY 421 CTCAATTCATCAGGCGGAGCTCATCTCACTGTCAACGAGCAGCAGCTGTATGGAT 480  
DB 421 CTCAATTCATCAGGCGGAGCTCATCTCACTGTCAACGAGCAGCAGCTGTATGGAT 480  
QY 481 ATGTTAGGCCAAGATGCGGTGATCGGTCTACTCTTCAAGCGGTGCGGTAAACGACCATTC 540  
DB 481 ATGTTAGGCCAAGATGCGGTGATCGGTCTACTCTTCAAGCGGTGCGGTAAACGACCATTC 540  
QY 541 ACCGAGAGGAATATGACGGCCATGAACCTCGATCGGAGACGATAGTTCTTACCTTGA 600  
DB 541 ACCGAGAGGAATATGACGGCCATGAACCTCGATCGGAGACGATAGTTCTTACCTTGA 600  
QY 601 AACTATACGATGTCGCGCGAGGTAGATCATCAGATTCTCAAGCTGATGTAGTGTGGT 660  
DB 601 AACTATACGATGTCGCGCGAGGTAGATCATCAGATTCTCAAGCTGATGTAGTGTGGT 660  
QY 661 GACGCTGTCTCAGCGCGGTCAAGTCAAGCTGCGGTCTTCTCAATTCAGCCCAAGGCC 720  
DB 661 GACGCTGTCTCAGCGCGGTCAAGTCAAGCTGCGGTCTTCTCAATTCAGCCCAAGGCC 720  
QY 721 ATGTACAGCTCAGGATGCTGTACCAAGCTCTTCAAGCTCAACAAAGTTCTGTGTCG 780  
DB 721 ATGTACAGCTCAGGATGCTGTACCAAGCTCTTCAAGCTCAACAAAGTTCTGTGTCG 780  
QY 781 ACTGACGATGCTCTTTTCGCGGTCTCATCTGGAATTCGGCTCTCGCGTGTCTCGAAGA 840  
DB 781 ACTGACGATGCTCTTTTCGCGGTCTCATCTGGAATTCGGCTCTCGCGTGTCTCGAAGA 840

QY 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 900  
DB 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 900  
QY 901 GTCTCGAACACTACCCAGGCTCTTTCAAAACATGACCTACCAACTCGACCATCGGC 960  
DB 901 GTCTCGAACACTACCCAGGCTCTTTCAAAACATGACCTACCAACTCGACCATCGGC 960  
QY 961 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCACGCTTCTGTTTTCAGAACTCGACCCC 1020  
DB 961 GAAATCGCAACAGAGTCACTCGGCGCAACAGCATCACGCTTCTGTTTTCAGAACTCGACCCC 1020  
QY 1021 GCGAGCATGCGCCAGCGAAACAGAGTCTCGGAGCTACCTGCGACCAACACCCGACAAG 1080  
DB 1021 GCGAGCATGCGCCAGCGAAACAGAGTCTCGGAGCTACCTGCGACCAACACCCGACAAG 1080  
QY 1081 TCCAAAGTATCCCTGAGCGCTGATGCGGACCCATCTACGAGCGTACCTGCGACCAACACCCGACAAG 1140  
DB 1081 TCCAAAGTATCCCTGAGCGCTGATGCGGACCCATCTACGAGCGTACCTGCGACCAACACCCGACAAG 1140  
QY 1141 GCCAAGTGGGACTCTGGGATTCAGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200  
DB 1141 GCCAAGTGGGACTCTGGGATTCAGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTG 1200  
QY 1201 AGACGCGCAATCTTTGAGCGCTTTGAGAGCTTGATGTACTTTATGCGCAAGAACCTGTAT 1260  
DB 1201 AGACGCGCAATCTTTGAGCGCTTTGAGAGCTTGATGTACTTTATGCGCAAGAACCTGTAT 1260  
QY 1261 GCGAGTTCCTGCGGCGCTTTCTCTGAGGATGAGGATATGAGCCGATTTGAAGGCGGAT 1320  
DB 1261 GCGAGTTCCTGCGGCGCTTTCTCTGAGGATGAGGATATGAGCCGATTTGAAGGCGGAT 1320  
QY 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTGTAG 1356  
DB 1321 AAGGAGTGGACCAAGTATGCGAGTACGTTGGTGTAG 1356

RESULT 2  
ADN37285  
ID ADN37285 standard; DNA; 1356 BP.  
XX  
AC ADN37285;  
XX 15-JUL-2004 (first entry)  
XX Trichothecene 3-O-acetyltransferase encoding DNA SEQ ID NO:29.  
XX maternal tissue; plant seed; plant;  
KW bifunctional alpha-amylase subtilisin inhibitor gene promoter;  
KW alpha-amylase inhibitor promoter; ASI promoter; plant protectant;  
KW virucide; vaccine; resistance; infection; *Fusarium graminearum*;  
KW trichothecene 3-O-acetyltransferase; enzyme; gene; ds.  
XX  
OS Gibberella zeae.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1356  
FT /\*tag= a  
FT /product= "Trichothecene 3-O-acetyltransferase protein"  
XX  
XX WO2004035790-A1.  
XX  
XX 29-APR-2004.  
XX  
XX 17-OCT-2003; 2003WO-AU001381.  
XX  
XX 17-OCT-2002; 2002AU-00952143.  
XX  
XX (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.  
XX (GRAI-) GRAINS RES & DEV CORP.  
XX  
XX Furtado A, Henry RJ;  
XX

WPI; 2004-348462/32.  
P-PSDB; ADN37286.

WFI; 2004-348482/  
P-PSDB; ADN37286.

Expressing nucleic acid or protein in a plant seed, useful in enhancing resistance of a plant against *Fusarium graminearum* and barley stripe mosaic virus, comprises expressing a bifunctional alpha-amylase subtilisin inhibitor promoter.

Claim 20; SEQ ID NO 29; 169pp; English.

The present invention describes a method for expressing nucleic acid or protein in the maternal tissue of a plant seed. The method comprises expressing isolated nucleic acid operably under the control of a bifunctional alpha-amylase subtilisin inhibitor (ASI) gene promoter that is operable in the maternal tissue. Also described: (1) a method of enhancing or conferring resistance of a plant against: (a) Fusarium graminearum (head scab); and (b) barley stripe mosaic virus (BSMV); (2) an isolated transformed wheat and barley seed that expresses isolated nucleic acid encoding respectively a plant defence protein and a BSMV coat protein or an inhibitory RNA that prevents, inhibits or reduces expression of a BSMV movement protein placed operably under the control of the ASI gene promoter where the seed exhibits enhanced resistance against Fusarium graminearum (head scab) and BSMV by virtue of the presence of the nucleic acid compared to an otherwise isogenic line that does not express the nucleic acid placed operably under the control of the ASI gene promoter; (3) a method of producing an immunogenic composition; (4) an immunogenic composition comprising the maternal tissue of a plant seed produced by a process that comprises performing the method of (1); (5) a method of enhancing the nutritional quality of a bran or animal fodder; and (6) an isolated bran or maternal tissue of a seed produced by a process that comprises performing the method of (5). The composition has plant protectant and virucide activities, and can be used in vaccines. The method is useful in expressing nucleic acid or protein in the maternal tissue of a plant seed. The method and ASI gene promoter are useful in enhancing or conferring resistance of a plant against Fusarium graminearum and BSMV and in enhancing the nutritional quality of bran or animal fodder. The seed or bran product and the composition are useful as an oral vaccine against infection in the gastrointestinal, respiratory and urogenital tracts. The present sequence encodes the Fusarium graminearum (*Gibberella zeae*) trichothecene 3-O-acetyltransferase, which is used in the exemplification of the present invention.

Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;

Query Match	100.0%	Score 1356;	DB 12;	Length 1356;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1356;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps

QY 1 ATGGCTTCAAGATACAGCTCGACACCCCTCGCCAGCTACCAGGCCTCCTTTCGATCTAC 60

Db  
1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGCCTCCTTTCGATCTAC 60

QY 61 ACCCAAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 12

Db 61 ACCCAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTCAGC 12

Qy 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGAGGCCAGGTC 18

Db 121 ACCTTCGAGCAAGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGTCCGAGGCCAGGTC 18

Qy 181 AAAGCCGAGGCATTAGCGAGGGAACACACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 24

D6 181 AAAGCCGAGGCATTAGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 24

241 G T T C C T C G I G T G T A G T G A A A G A C C T C C G C G A T G A T C C T T C A G C G C C C A C G A T C G A G G G T 300  
QY

DB 241 G T T C C T C G T G T G T A G T G A A A G A C C T C C G C G A T G A T C C T T C A G C G C C C A C G A T C G A G G G T 30

QY 301 A T G A G A T A G G C G G G A T A C C C A T G G C G A T G T T T G A C G A G A A C A T C T C G C C A G A G A A G 308

DD JVI AIGAGTAAGCGCGGATAACCTATGGCGATGTTGACGAGAACATCATCGCGCAAGGAGAG 38

### RESULT 3

AAZ89368

yy ID AAZ89368 standard; DNA; 1605 BP.

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AAZ89368;  
15-SEP-2003 (revised)  
09-JUN-2000 (first entry)  
F. graminearum trichothecene 3-O-acetyltransferase DNA.  
Trichothecene 3-O-acetyltransferase; selective marker; ds.  
Gibberella zeae.  
Key Location/Qualifiers  
CDS 135..1490  
/\*tag= a  
/product= "trichothecin 3-O-acetyltransferase"  
JP2000032985-A.  
02-FEB-2000.  
15-JUL-1998; 98JP-00200280.  
15-JUL-1998; 98JP-00200280.  
(RIKA ) RIKAGAKU KENKUSHO.  
(YAMA/) YAMAGUCHI I.  
WPI; 2000-274037/24.  
P-PSDB; AAY51848.  
Trichothecin 3-O-acetyltransferase gene useful as a selective marker in  
gene manipulations in eukaryotic host cells.  
Claim 3; Page 16-18; 25pp; Japanese.  
This invention describes a novel protein with trichothecin 3-O-  
acetyltransferase activity. The gene is used as a selective marker in a  
gene manipulation using eukaryote as the host cell. This sequence encodes  
the trichothecin 3-O-acetyltransferase isolated from Fusarium  
graminearum. (Updated on 15-SEP-2003 to standardise OS field)  
SQ Sequence 1605 BP; 397 A; 459 C; 393 G; 356 T; 0 U; 0 Other;  
Query March 98.8%; Score 1340; DB 3; Length 1605;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
1 ATGGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACGAGCCTCTTCGATCTAC 60  
135 ATGGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACGAGCCTCTTCGATCTAC 194  
61 ACCCAATCAGTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGC 120  
195 ACCCAATCAGTCTCTACCCCGTCTCTGATCCCTCTCAATATCCCACTATTGTTCAGC 254  
121 ACCTTCGAGCAAGGTCTTAAGCGTCTTCGAAAGCGCTCCCATGGGTCGAGGCCAGGTC 180  
255 ACCTTCGAGCAAGGTCTTAAGCGTCTTCGAAAGCGTCTCCCATGGGTCGAGGCCAGGTC 314  
181 AAAGCCGAGGGCATTTAGCGAGGGAACAACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 240  
315 AAAGCCGAGGGCATTTAGCGAGGGAACAACAGGAACCTTCCTTTATCGTCCCTTTTGAGGAC 374  
241 GTTCTCTGTTGTAGTCAAGACCTCGCGATGATCTTCAGCGCCCAACGATCGAGGGT 300  
375 GTTCTCTGTTGTAGTCAAGACCTCGCGATGATCTTCAGCGCCCAACGATCGAGGGT 434  
301 ATGAGAAAGGGGGATACCTATGCGGATGTTTGAACGAAACATCATCGGCCCAAGGAAG 360  
435 ATGAGAAAGGGGGATACCTATGCGGATGTTTGAACGAAACATCATCGGCCCAAGGAAG 494  
361 ACGTTACCTATTGGACCTGGTACTGGTCCGAGACCAAGACCTGTAAATTCTATTGCGAG 420

Db 495 ACGTTACCTATTGGACCTGGTACTGCGCCCGCAGCAGCCAAAGCCTGTGATTCATTGCGAG 554  
Qy 421 CTCAACTTTCATCAAGGGCGGACTCATCTCAGTGTCAACGAGCAGCAGCGGTCTATGGAT 480  
Db 555 CTCAACTTTCATCAAGGGCGGACTCATCTCAGTGTCAACGAGCAGCAGCGGTCTATGGAT 614  
Qy 481 ATGTTAGGCCAAGATGCGGTGATCCGTTACTCTCTCAAGGCGTGCCTTAACGCCCATTC 540  
Db 615 ATGTTAGGCCAAGATGCGGTGATCCGTTACTCTCTCAAGGCGTGCCTTAACGCCCATTC 674  
Qy 541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAGAGCATGTTCTTCACTTACCTTGA 600  
Db 675 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAGAGCATGTTCTTCACTTACCTTGA 734  
Qy 601 AACTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGT 660  
Db 735 AACTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGT 794  
Qy 661 GACGCTGTTCTCAGCGCCGTCAGTGCAGGCTGGGGTCTTCTCACTTCACTTCACTTCA 720  
Db 795 GACGCTGTTCTCAGCGCCGTCAGTGCAGGCTGGGGTCTTCTCACTTCACTTCACTTCA 854  
Qy 721 ATGTCAAGCTCAAGGATGCTGTACCAAGCTGTTCGACGATCAACAAAGTTCTGTCTCG 780  
Db 855 ATGTCAAGCTCAAGGATGCTGTACCAAGCTGTTCGACGATCAACAAAGTTCTGTCTCG 914  
Qy 781 ACTGACGATGCTCTTTTCGGGCTTTCATCTGGAATTCGGCTCTCTCGCTGCGTCTCG 840  
Db 915 ACTGACGATGCTCTTTTCGGGCTTTCATCTGGAATTCGGCTCTCTCGCTGCGTCTCG 974  
Qy 841 ATCGATGGCTCTGCACTTACCGGATCTGCGGCTGCTGTGATGCTGCGACCGGCAATGGT 900  
Db 975 ATCGATGGCTCTGCACTTACCGGATCTGCGGCTGCTGTGATGCTGCGACCGGCAATGGT 1034  
Qy 901 GTCTCGAACAACCTACCGAGGCTTCTTCAAAACATGACCTACCAACAACCTCGACCATCG 960  
Db 1035 GTCTCGAACAACCTACCGAGGCTTCTTCAAAACATGACCTACCAACAACCTCGACCATCG 1094  
Qy 961 GAAATCGCAACGAGTCTCTCGGCGCAACAGCATCAGCCCTCGTTCAGAACTCGACCCC 1020  
Db 1095 GAAATCGCAACGAGTCTCTCGGCGCAACAGCATCAGCCCTCGTTCAGAACTCGACCCC 1154  
Qy 1021 GCGAGCATGCGCCGCAAGAGGCTCTCGGAGTACCTGCGACCAACAACCCCGACAAAG 1080  
Db 1155 GCGAGCATGCGCCGCAAGAGGCTCTCGGAGTACCTGCGACCAACAACCCCGACAAAG 1214  
Qy 1081 TCCAAAGTATCCCTCAGCGGCTGATCGGAGCCCATCTACCGGCTCATGCTGAGTCTTTGG 1140  
Db 1215 TCCAAAGTATCCCTCAGCGGCTGATCGGAGCCCATCTACCGGCTCATGCTGAGTCTTTGG 1274  
Qy 1141 GCGAAGGTGGGACTCTCGGATTAACGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200  
Db 1275 GCGAAGGTGGGACTCTCGGATTAACGCTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1334  
Qy 1201 AGACGCGCAACTCTTTGAGCTGTTGAGGCTGTTGAGGCTTGTATGTTATGCCCAAGAGCTGAT 1260  
Db 1335 AGACGCGCAACTCTTTGAGCTGTTGAGGCTGTTGAGGCTTGTATGTTATGCCCAAGAGCTGAT 1394  
Qy 1261 GCGGAGTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGACCGATTTGAAGCGGGAT 1320  
Db 1395 GCGGAGTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGACCGATTTGAAGCGGGAT 1454  
Qy 1321 AAGGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1356  
Db 1455 AAGGAGTGACCAAGTATGCGCAGTACGTTGGTTAG 1490

RESULT 4  
AA54206  
ID AAA54206 standard; cdna; 1403 BP.  
XX  
AC  
AA54206;  
XX

DT	26-FEB-2001	(first entry)	
DE	Sequence encoding trichothecene resistance polypeptide.		
XX			
KW	Trichothecene resistance; resistant; crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; transformation; Fusarium; ds.		
XX			
OS	Fusarium sporotrichioides.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	7..1386	
FT	/*tag= a		
FT	/product= "Trichothecene resistance polypeptide"		
XX			
PN	W0200060061-A2.		
XX			
PD	12-OCT-2000.		
XX			
PF	29-MAR-2000; 2000WO-EP002769.		
XX			
PR	31-MAR-1999; 99US-00282995.		
PR	11-FEB-2000; 2000US-00502852.		
XX			
PA	(NOVS ) NOVARTIS AG.		
PA	(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX			
PI	Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;		
XX			
DR	WPI; 2000-679374/66.		
DR	P-PSDB; AAB03934.		
XX			
XX	Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity.		
XX			
PS	Claim 8; Page 46; 62pp; English.		
XX			
CC	A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation		
XX			
SQ	Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 U; 0 Other;		
Query Match 67.5%; Score 915.6; DB 3; Length 1403;			
Best Local Similarity 80.3%; Pred. No. 1.1e-278;			
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
Qy	3	GGCTTTCAAGATACAGCTCGACCCCTCGGCGAGCTACGAGGCTCCTTTTCGATCTACAC	62
Db	36	GTCTTTTGATAGAGCTCGACATCATCGGCGAGCAACCGGCTCTCTTTCAATCTACAC	95
Qy	63	CCAAATCAGTCTCTTACCCGCTCTGATTCCTCTCAATATCCCACTATTGTACGACAC	122
Db	96	CCAGATCAGTCTCGTTTACCCGCTCTGATCCCTCCAGTATCCCACTCTGTGAGCAC	155
Qy	123	CTTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGTCCCATGGGTCCGAGGCCAGGTCAA	182
Db	156	CCTTGAGGAAGGCTTAAGCGCTCTCTCAAACTTCCCATGGGTCCGCGGCCAGGTCAA	215
Qy	183	AGCCGAGGGCATTTAGCGAGGGAACAACAGGAACCTTCTTTATCGTCCCTTTTGAGGACGT	242
Db	216	GACCGAGGGCATTCAGCGAAGGGAACAACAGGAACCTTCCAAGATCATTTCCATATGAGGAGAC	275
Qy	243	TCCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTTCAGGCCCCACCATCGAGGGTAT	302
Db	276	ACCCCGTCTTGTGGTGAAGACCTCCGTGATGATTCCTCAGCGCCCAACGATCGAGGGGTT	335

Qy	303	GAGAAAGCGGGATACCTATGCGCATGTTTGACGAGAAACATCATCGCCCGCAAGGAGAC	362
Db	336	GAGAAAGCGGGTTCCTCCCTTAGAGATGTTTGACGAGAAACGTCGTCGCTCCGAGGAGAC	395
Qy	363	GTTACTATTGACCTGGTACTGGTCCGACCAACCAAGCTGTAAATCTTATTGAGCT	422
Db	396	ATTAGCTATCGACCTGGCAATGGCCCAACGACCGAAGCTGTGTTGCTATTGAGCT	455
Qy	423	CAACTTTCATCAAGGCGGACTCATCTCTCACTGTCAACGAGACGAGTGTGATAT	482
Db	456	CAACTTTCATTAAGGCGGACTCATCTCTCAACGAGCAACATGGTGTATGGACAT	515
Qy	483	GATAGCCCAAGATCGGTGATCCGTCTACTCTCAAGGGGTGCGTAAGCAACCCATTAC	542
Db	516	GACAGGACAAGATGCAATTAATTCGTCTCTCCAAAGGCGTCCGCAACGAATATTAC	575
Qy	543	CGAAGAGGAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA	602
Db	576	CGAGGAGGAATCTCGGCATGAACTCGATCGCAAGACGATAGTTCCTTCTTGA	635
Qy	603	CTATACGATTGGCCCGGAGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGTA	662
Db	636	CTACAAAGTTGGTCTCTGAGCTAGACCAGATGCCAAACC--TGCGCTGCTGGCGA	692
Qy	663	CGCTGTTCTCAGCCGGTCAAGTGGGGTTCCTTCAATTCAGATTCAGCCCAAGCCAT	722
Db	693	CGCTCCACCCGCAAGGCAAGCTGGGGTTCCTTTCATTCATCTCCCAAGCCCT	752
Qy	723	GTGAGAGCTCAAGGATGCTTACCAAGACTCTTCAGGCAACAAAGCTTCGTGTGAC	782
Db	753	CTCGAGCTGAAAGACGCGACCAAGAACTCTTGACGGCTGTCAGATTTGTGTCAAC	812
Qy	783	TGACGATGCTCTTTTGGGGTTCATCTGGAATTCGGCTCTCGCGTGGCTCTCGAAGAT	842
Db	813	TGATGATGCTCTTTGGGGTTCATCTGGAATTCGGCTCGCGTGGCTCTCGAAGAT	872
Qy	843	CGATGCTCTGACCTACGAGTTCGCGTCTGTTGATGCTCGACCGGCAATGGGTGT	902
Db	873	GGATGCTTCCACACTCTGAAATTCGCGCTGTCGACATCGCGGGGCCAATGGGCT	932
Qy	903	CTCGAAGCACTACCGAGCTCTTTCAAACATGACCTACCAACCTCGACCATCGGCGA	962
Db	933	ATCAAGCACTACCGAGCTCTTTCAAACATGACCTACCAACCTCGACCATCGGCGA	992
Qy	963	AATCGCAACGAGTCACTCGGCGCAACGATCAGCCCTTCGTTTCAAGAACTCGACCCCG	1022
Db	993	AATCGCAACGAACTTGGCGCAACGATCAGCCCTCGCTCGGAACCTCAACAGTGA	1052
Qy	1023	GAGCATGCGCCAGCAACGAGGTCTCGGACGTCTCGGACATCTGCAACCAACCCGCAAGTC	1082
Db	1053	TCGTTTGGCGAGCAACAAAGCTTTGGCGACGTACATGCAATGCGCTCGTCAAGTC	1112
Qy	1083	CAAGCTATCCCTGACGGCTGATCGGACCCATCTACGAGCTCATGCTCAGTCTTTGGGC	1142
Db	1113	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCAGAGACATCATGCTGAGTCTTGGGC	1172
Qy	1143	CAAGTGGGACTCTGGGATTAACAATTTGGGCTCGGACTCGGTTAAGCCCGAGATGTGAG	1202
Db	1173	CAAGTGGGATCTGGGATGATGATCTTTGGGTTTGAGCTGGGTAGGCTGAGATGTGAG	1232
Qy	1203	ACGGCAATCTTTGAGCTGTTGAGAGCTTGATGATCTTTATGCCCCAAGAGCTGATGG	1262
Db	1233	AAGACTCTGCTTGAACCTTTTGAAGTGTGATCTTTATGCCCCAAGAGCTGATGG	1292
Qy	1263	CGAGTCTGTGCGGCTTCTCTGAGGATGAGGATGAGCCGATTCAGAGCGGATAA	1322
Db	1293	GGAGTTTACGGGCTCAATTTCTCTGAGGATGAGGATGAGGACTTAAGCGGATGA	1352
Qy	1323	GGAGTGGACCAAGTATGCGCAGTATGCTTGGTTAG	1356
Db	1353	GGAGTGGACCAAGTATGCGCAAGATATATTTGGGTAG	1386



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RESULT 5	243	TCCTCGTGTGTAGTGAAGACCTCCGCGATGATCTTACGCGCCCAACGATCGAGGTAT	302
AAA54213	11521	ACCCGTCCTTGTGTGAAGACCTCCGCGATGATCTTACGCGCCCAACGATCGAGGTAT	11580
ID AAA54213 standard; DNA; 12949 BP.			
XX			
AC AAA54213;	303	GAGAAAGCGGGATACCCCTATGGCGATGTTTACGAGAACATCATCGCGCAAGGAGAC	362
XX			
DT 26-FEB-2001 (first entry)	11581	GAGAAAGCGGGTTCCTCCCTTAGAGATGTTTACGAGAACCTGCTCGGAGGAGAC	11640
XX			
Transformation vector pNOV1704.	363	GTTACCTATTGGACCTGTACTGTCGCGACGACCCAAAGCCCTGTAATCTATTTCAGAGCT	422
XX			
DE Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;	11641	ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAAGCCCTGTGTGCTATTTCAGCT	11700
XX			
KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;	423	CAACTTCATCAAGGGCGGACTCATCTCTCACTGTCAACGAGCAGCAGCTGTCTATGGATAT	482
XX			
KW ds.	11701	CAACTTCATTAAAGGCGGACTCATCTCTCACTGTCAACGAGCAGCAGCTGTCTATGGATAT	11760
XX			
OS Synthetic.	483	GGTAGGCAAGATCGGTGATTCGCTCTCTTCCAGGCGTGGCGTAAGACCCATTTCAC	542
XX			
PN W0200060061-A2.	11761	GACAGGCAAGATGCAATTTATTCGCTCTCTTCCAGGCGTGGCGTAAGACCCATTTCAC	11820
XX			
PD 12-OCT-2000.	543	CGAAGGGAATGACGGCCATGAACTTCGATCGCAAGACGATAGTTCCTTACCTTGAATA	602
XX			
PF 29-MAR-2000; 2000WO-EP002769.	11821	CGAGAGGAATCTCGGCCATGAACTTCGATCGCAAGACGATAGTTCCTTACCTTGAATA	11880
XX			
PR 31-MAR-1999; 99US-00282995.	603	CTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGTGTGTA	662
XX			
PR 11-FEB-2000; 2000US-00502852.	11881	CTACAAAGTTGCTCTGAGCTAGACCACCAAGATCGCAAAACC--TGCCTGCTGTGCGA	11937
XX			
XX (NOVS ) NOVARTIS AG.	663	CGCTGTTCTCAGCGCGGTGATGCAAGCTGGCGCTTCTTCACTTACGCCCCAAGGCGAT	722
XX			
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.	11938	CGCTCACCACCGGCAAGGCAAGCTGGCGCTTCTTCACTTACGCCCCAAGGCGAT	11997
XX			
PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;	723	GTGAGAGCTCAAGGATGCTGTACCAAGACTCTTTGAGCGATCAACAAAGTTGTTGCGAC	782
XX			
DR WPI; 2000-679374/66.	11998	CTCGAGCTGAAGAGCAGCAGCAAGACTCTTTGAGCGCTGCTCAAGTTTGTGTCAAC	12057
XX			
XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley	783	TGACGATGCTCTTTCGGGCTTCATCTGGAATCGGCTCTCGCGTGGCTCTCGAAGAAAT	842
XX			
PT or rice plant, comprises heterologous polynucleotide encoding gene	12058	TGATGATGCTCTTTCGGGCTTATCTGGAATCAACCTCGCGCTGCTCTCGAAGATT	12117
XX			
PT product expressed in cell, having tricothecene resistance activity.	843	CGATGGCTTCGACCTACCGAGTTCTGCGTGTGTGATGCTCGACCGGCAATGGGTGT	902
XX			
XX Disclosure; Page 58-62; 62pp; English.	12118	GGATGCTTCCACACTACTGATTTCTGCGGCTGTGCACATGCGGGGCCCAATGGGCT	12177
XX			
XX A heterologous gene encoding a gene product which confers tricothecene	903	CTCGAACAACCTACCGAGCTTCTTCAAAATGATGCTTACCAACTGACATCGCGCA	962
XX			
CC resistance can be used to transform plant cells to make them resistant to	12178	ATCAAGCACATACCCAGGCTTCTTCAAAATGATGCTTACCAACTGACATCGCGCA	12237
CC fungal infection. The transformation method is useful for preventing	963	ATTCGCCAACGAGTCACTCGCGGCAACAGCATCAGCGCTTCTGTTGAGAACTCGACCCGCG	1022
CC mycotoxin contamination of a plant, particularly a crop plant such as	12238	AATCGCCAAACGAAACCATTTGGCGCAACAGCATCAGCGCTGCTCGGAACTCAACAGTGA	12297
CC wheat, maize, barley or rice, and for reducing and/or preventing the	1023	GAGCATGCGCCAGCGAAACAAAGAGGTCTCGCGAGTCTCGCACAAACCCCGCAAGTTC	1082
CC growth of a fungus of the genus Fusarium that produces a tricothecene,	12298	TGCTTTGCGCACACGACACACAGCTTTGCGAGGTACATGATGCGCTGCTGCAAGTTC	12357
CC preferably comprising a C-3 hydroxyl group, by growing transformed crop	1083	CAAAGTATCCCTGACGGGTGATGCGGACCCATCTACAGCGCTCATGCTGAGTTCTTGGGC	1142
CC plants in an area which is moderate to severe fungal infestation. Plasmid	12358	GAGCGTCTCCCTGACCGCGATGCGAATCCGTCGCAAGCAGCATCATGCTGAGTTCTTGGGC	12417
CC pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose	1143	CAAGTGGGACTCTGGGATTTAGAGCTTTGGGCTCGGACTTGGGTAAAGCCCGAGACTGTGAG	1202
CC isomerase selectable marker and the nopaline synthase termination	12418	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTGAGCTGGGTGAGGTGAG	12477
CC sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter	1203	ACGGCCAAATCTTTGAGCCTGTTGAGAGCTTGATGATCTTTATGCGCCAAAGACCTGATGG	1262
CC operably linked to the tricothecene 3-O-acetyl transferase sequence	12478	AAGACCTCGCTTTGAACCTTTTGAAGTTTGAATCTTATGCGCCAAAGACCTGATGG	12537
CC given in GENESEQ record AAA54206 and the nos termination sequence	1263	CGAGTTCTGTGGCGCTTCTCTGAGGATGATGAGGATGAGGATGAGGCGGATAA	1322
XX			
XX Sequence 12949 BP; 3194 A; 3146 G; 3143 G; 3466 T; 0 U; 0 Other;	12538	GGAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATGAGGATGAGGCGGATGA	12597
XX			
XX Query Match 67.5%; Score 915.6; DB 3; Length 12949;			
XX			
XX Best Local Similarity 80.3%; Pred. No. 3.7e-278;			
XX			
XX Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
QY 3 GCGTTTCAAGATACAGCTCGACACCTCGGCGAGCTACCGGCTCTCTTTCGATCTACAC	62		
DB 11281 GTCTTTTGACATGAGCTCGACATCATCGGCGCAACCGGCTCTCTTTCATCTACAC	11340		
QY 63 CCAATACGTCCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGAGCAC	122		
DB 11341 CCAATACGTCCTGTTTACCCCGTCTCTGATTCCTCCAGTATCCCACTATCGTCAGCAC	11400		
QY 123 CTTGAGCAAGTCTTAAGCGCTTCTCGAAGCGCTTCCATGGTTCGAGCCAGGTCAA	182		
DB 11401 CTTGAGCAAGGCTTAAACCGCTCTCTCAACCTTCCATGGTTCGAGCCAGGTCAA	11460		
QY 183 AGCCGAGGCTATTAGCGAGGGAACACAGGAACCTTCTTTATCGTCCCTTTTGAAGACGT	242		
DB 11461 GACCGAGGCGATCAGCGAAGGAACACAGGAACCTTCCAGATCATTCATATGAGGAGAC	11520		





QY 1263 CGAGTTCTGTGGCGCTTTCTCTGAGGATGAGATATGGACCGATTGAGGCGGATAA 1322  
 Db 1307 GGAGTTTACGGCGCTCCATTCTCTGAGGATGAGATATGGAGACTAAAGCGCGATGA 1366

QY 1323 GGAGTGGACCAAGATATGCGCAGTACGTTGGTTAG 1356  
 Db 1367 GGAGTGGACCAAGATATGCGCAGTATATGGGTAG 1400

## RESULT 7

AA54210  
 ID AA54210 standard; DNA; 1425 BP.

AC AA54210;

XX 26-FEB-2001 (first entry)

DE Sequence encoding trichothecene resistance polypeptide.

XX Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;  
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
 KW ds.

XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers

FT CDS 1. 1425

FT /\*tag= a

FT /product= "Trichothecene resistance polypeptide"

XX W0200060061-A2.

PN 12-OCT-2000.

XX 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.

DR P-PSDB; AAB03936.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
 or rice plant, comprises heterologous polynucleotide encoding gene  
 product expressed in cell, having trichothecene resistance activity.

XX Claim 8; Page 50-51; 62pp; English.

XX A heterologous gene encoding a gene product which confers trichothecene  
 resistance can be used to transform plant cells to make them resistant to  
 fungal infection. The transformation method is useful for preventing  
 mycotoxin contamination of a plant, particularly a crop plant such as  
 wheat, maize, barley or rice, and for reducing and/or preventing the  
 growth of a fungus of the genus Fusarium that produces a trichothecene,  
 preferably comprising a C-3 hydroxyl group, by growing transformed crop  
 plants in an area which is moderate to severe fungal infestation

SQ Sequence 1425 BP; 431 A; 305 C; 293 G; 396 T; 0 U; 0 Other;

Query Match 18.4%; Score 249.8; DB 3; Length 1425;

Best Local Similarity 51.9%; Pred. No. 7.7e-68;

Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGTCGACACCCCTCGGCGACGTACCGGCTCTCTTCGATCTACACCCAAATCAGTCTC 75

Db 64 CAACCTGATATTTGGGACACACACCTTCGCTATACAACTATACATCAATATGCTCT 123

QY 76 CTCTACCCCGTCTCTGATTCTCTCAATATCCCACTATTGTCTCAGCACCTCTCGAGCAGGT 135  
 Db 124 ATCTACCGTGTACAGATCTCTCTGCTCATGACCATTATCGTAATACCTTAACAAGAGGA 183  
 QY 136 CTTAAGCGCTTCTCCGAAGCGCTCCCATGGTGCAGGCCAGGTCAAAGCCGAGGCGATT 195  
 Db 184 CTTGAAACATTGGCTAAATAATTTCCAGTGGCTAGCAGGAAATGTCTGTAATGAAGTGTCT 243  
 QY 196 AGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTTGAGGACGTTCTCTGTTGTTGA 255  
 Db 244 GACGAAGGTAACTGTGTACTACAGAAATGTCCCGTCAGACAAAATTCACAC---TTATC 300  
 QY 256 GTGAAAGACCTCCCGATGATCTCTTACGCCGCCACGATCGAGGATGAGAAAGCCGGA 315  
 Db 301 GTCCAAGATCTTCGAGAAGATCTGTCTGCCCAACAATGGATTTCGCTTGAAGAGCTGAC 360  
 QY 316 TACCTATGGCGATGTTTGACGAGAACATCATCCGCCCAAGGAAGAGCTT-----ACCT 369  
 Db 361 TTCTCTATCTACATGTTAGACGAAAAGACTTTTGGCTTGCATGACTATCAATCCACCT 420  
 QY 370 ATTGACCTGTGTAATGTTCCGACGCCAACAAAGCTGTAAATTTCTTATTTGACGCTCAACTTC 429  
 Db 421 GGAAACACTATAGGTATGGCCGCCCAAGAGTGGGCTGTATTGTCAGTTCAAGCAAACTTT 480  
 QY 430 ATCAAGGCGGACTCATCTCCTCACTGTCAA CGGACAGCACGGTGTCTATGATATGTTAGGC 489  
 Db 481 ATCTCCGGCGGCTCGTCTTAACATATTGTTCGGGAGCACAATATTATGATATTAACAGGA 540  
 QY 490 CAAGATGCGGTGATCCGCTCTACTCTCCAAAGCGTGGCGGTACGACCCATTCACCGAAGAG 549  
 Db 541 CAGGAAAGTATCACTCACTTGTCTCAATAAATCTTGCCACCAAAACCTTTCTCTGATGAA 600  
 QY 550 GAAATGACGGCCATGAACCTCGATCGAAGACGATAGTTCCTTACCTTGAATAACTATACG 609  
 Db 601 GAACCTGCTCATTTGGAAATATAGATAAAAGCAAACTATTCTCTTTGTTGATGAACCTTTGG 660  
 QY 610 ATT----GGCCCGAGGTAGATCATCAGATTCTCAAGCTGATGATGCTGGTGGTACGCT 666  
 Db 661 GAAACCCGACACACGCTAGTTCATGAAATAGTGGAAACCTCTAGAAATACAGTGGAGAG 720  
 QY 667 GTTCTCAGCGCGGTCACT-----GCAAGCTGGGCGTCTTTCACATTCAGCCCCAAG 717  
 Db 721 GAAAGGAAACAGTCTTGTCTTCGAACCTACTTGGGCTTATGTTGAATTTTCTGCTATC 780  
 QY 718 GCATGTACAGCTCAAGATGCTCTACCAAGATCTTGACGCTATCAACAAAGTTCGTG 777  
 Db 781 TCATTGCAGAAATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840  
 QY 778 TCGACTGACGATGCTCTTTGGCGTTCATCTGGAATCGGCTCTCGGCTGGCTCGAA 837  
 Db 841 TCCACTGATGATATCGTCACTGCTTTTCACTGGAATCAGTTTCTCGAGCCGTTTATCT 900  
 QY 838 AGAATCGATGGCTCTGCGACCTACCGAGTTCTGCCGTGCTGTTGATGTCTGACCCGCAATG 897  
 Db 901 CGACTTAAACAGAAACGAAATCAAATTTAGGGCGTCTGTGATGTTAGAAAACGGCTTA 960  
 QY 898 GGTGTCTGAACAACTACCCAGGCTTCTTCAAAACATGACCTTACCAACTCGACCATC 957  
 Db 961 GGACTCCCGAAAACGTTATTCAGGGTTATTAGTCAACATGACCTTTAAATACAGTTCCCTG 1020  
 QY 958 GCGGAAATCGCAACGAGTCACTCCGCGCAACAGCATCACGCTTCTGTTTCAGAACTCGAC 1017  
 Db 1021 AAAAGCTTGATCATAAAGTTTGGCGGCTTCTGATCAGATTCGAGGAAGCTAGAC 1080  
 QY 1018 CCGCGGAGCA-----TGCGCCAGGGAACAAAGGTCTCGGACGTCTCGCACACACAC 1071  
 Db 1081 CCTAAAGTCTTCGATTTGGCTTATAATCATGCGACCTTGTACGCTCTCTTAGCCGATGC 1140  
 QY 1072 CCGGACAAAGTCAACGATATCCCTGAGCGGTGATGGGACCCATCTACACAGCGTCACTGCTG 1131  
 Db 1141 CCGGACAAAGCTAAAGTTTCTATACCTCAACCAATGATCTTATCTCGAATATGGTCT 1200  
 QY 1132 AGTTCTTGGGCCAAAGGTGGGACTCTGGGATTACGATTTTGGGCTCGGACTGGGTAAAGCCC 1191

Db	1201	AGTTCTGTGGGCAAAAGTCAGCCTGTATGACGTTGATTTCAATCTAGGCGTTGGGAAGCCC	1260
Qy	1192	GAGACTGTGAGACGGCCCAACTCTTTGAGCCCTGTTGAGAGCTTGATGTACTTTATGCCCCAAG	1251
Db	1261	AAGAGTGTACGACGGCCGCGCTTCATTTCCCTTGAGAGCCTAATATATTTATTTATGCTCTAGA	1320
Qy	1252	AAGCCTGATGCGCAGTTCGTGCGGCGCTTCTCTGAGGGATGAGGATATGGACCGATTG	1311
Db	1321	TCCTCCAGAGGTGAAATGGTGGTTGCTCTTTGCCCTTAGAGATTAAGATTCGGAGTGCCTG	1380
Qy	1312	AAGCGGATGAAGGAGTCGACCAAGTATGC	1340
Db	1381	AATCGCGATAAAGAATATGGACAAATTTATGC	1409

RESULT 8	
AAAF12071	
ID	AAAF12071 standard; cDNA; 695 BP.
XX	
XX	AAAF12071;
XX	
XX	
DT	13-MAR-2001 (first entry)
XX	
DE	Aspergillus oryzae EST SEQ ID NO:4594.
XX	
XX	
KW	Multiple gene expression; filamentous fungal cell; EST;
KW	expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW	Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW	culture condition; environmental stress; spore morphogenesis;
KW	metabolic pathway engineering; catabolic pathway engineering; ss.

CC	products to facilitate analysis of the results. AAF07478 to AAF11247
CC	represents ESTs from <i>Fusarium venenatum</i> ; AAF11248 to AAF11853 represents
CC	ESTs from <i>Aspergillus niger</i> ; AAF11854 to AAF14878 represents ESTs from
CC	<i>Aspergillus oryzae</i> ; and AAF14879 to AAF15337 represents ESTs from
CC	<i>Trichoderma reesei</i> , which are all specifically claimed in the present
CC	invention
XX	
SQ	Sequence 695 BP; 174 A; 191 C; 156 G; 172 T; 0 U; 2 Other;
	Query Match            10.8%; Score 146.2; DB 3; Length 695;
	Best Local Similarity 57.5%; Pred. No. 3.4e-35;
	Matches 325; Conservative 0; Mismatches 225; Indels 15; Gaps 3;
QY	5 CTTTCAAGATACAGCTCGACACCCTGCGCAGCTACACGGCCTCTTCGTGATCTACACCC 64
Db	
	109 CATTAATGATAAAGCTGAACCTTCGTGGTCAGCTGCCTGCCCTC--AGGATCTACACGC 165
QY	65 AAATCATGTCCTCTACCCCGTCTCTGATTCTCTCAATATCCCACATATTGTTCAGCACCT 124
Db	
	166 AAATCTGCCCTCTGCTTTCCGCTC--GATGCCCTCATGTATCAGGATAGTAGCAGACCC 222
QY	125 TCGAGCAAGGCTTTAAAGCGCTTCTCGGAAGCCGTCCTCATGGTGCGCAGGCCAGCTCAAAG 184
Db	
	223 TAGGAATGGCTCGAAGAAGACTGTCACCAATTTCCGTGGGTAGCAGGCCAGATAGTCA 282
QY	185 CCAGGGGCATTACGAGGGAAAAACAAGGAACCTTCCTTTTATCGTCCCTTTTGAGGACGCTC 244
Db	
	283 GTGAAGGCAGCAGCCACAACAATCCTGGCACATTCATGATCAAAGCACTCGGGAAGACTC 342
QY	245 CTGCTGTGTAGTGAAGACCTCGCGATGATCCTTCAGCGCCACAGCATCGAGGGTATGA 304
Db	
	343 CACCACCTGGTTGTGAAGACTTCCGTCATGATCCGACGTTCCGACCATGGACGATTTGA 402
QY	305 GAAAAGGGGGATACCCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAGACGT 364
Db	
	403 GACGCGCGACTTTCCTTTTCGAGATTAGACGAGAACATCATTTGCTCTCGGNAACCT 462
QY	365 TACCTATTGACCTGGTGTGTCGCCGACGCCAACCCGCTGTAATTCTATTTCAGCTCA 424
Db	
	463 TGCCAA-----GCCCTGACGAAGATATTATCTCACCGGCTTTCTTGTCAGGCTA 513
QY	425 ACTTCAATCAAGGGGGAACCTCATCTCACTGTCAACGGACAGCAGGTGCTATGGATATGG 484
Db	
	514 ATTNTATTACGGCGGGCTGTGCTCCTCACTCTTTGTGGCCAATCATAGCAATGGACATGA 573
QY	485 TAGSCCAAGATCGGTGATCCGCTCACTCTCCAAGGGTCGCTTAACGACCCCATTTACCG 544
Db	
	574 CTGGTCANGACAGGTTATCCACCTTCTCTCGAAGGCATGTCGTGGGATACATATACAA 633
QY	545 AAGAGGAAATGACGGGCCATGAACCT 569
Db	
	634 GATTGGAGCTAGAGTCAGGGAACCTT 658
RESULT 9	
ABZ54817	
ID	ABZ54817 standard; cDNA; 482 BP.
XX	
AC	ABZ54817;
XX	
DT	28-MAR-2003 (first entry)
XX	
DE	<i>Aspergillus oryzae</i> polynucleotide SEQ ID NO 3930.
XX	
KW	<i>Aspergillus oryzae</i> ; fermentation; fungus; industrial; EST;
KX	expressed sequence tag; gene; ss.
OS	<i>Aspergillus oryzae</i> .
PN	WO200279476-A1.
PD	10-OCT-2002.
XX	

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PF 22-MAR-2002; 2002WO-IB000890.
XX
PR 30-MAR-2001; 2001JP-00098371.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NOR-) NAT FOOD RES INST MIN AGRIC.
XX
XX Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
XX
XX WPI; 2003-046817/04.
DR
XX
XX Detection of expression of specific Aspergillus genes for monitoring the
PT fermentation and growth conditions of the fungus, using DNA probes.
XX
XX Claim 1; SEQ ID NO 3930; 48pp + Sequence Listing; Japanese.
XX
XX The invention relates to a polynucleotide having any of 6006 specific
CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
CC specific culture conditions including one or more of eutrophic,
CC oligotrophic, solid, early germination, alkaline, high temperature, low
CC temperature or maltose culture or polynucleotides stringently hybridising
CC to these sequences. The polynucleotides are useful for monitoring the
CC progress of fermentation and the growth conditions of a fungus,
CC especially of Aspergillus oryzae which is widely used in industrial
CC fermentation. Also monitoring for fungal contamination. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 482 BP; 131 A; 109 C; 115 G; 127 T; 0 U; 0 Other;
SQ
Query Match 8.6%; Score 116.2; DB 8; Length 482;
Best Local Similarity 60.1%; Pred. No. 8.8e-26;
Matches 193; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 1036 CGAACAGAGGTCTCGCGAGTACCTCGCACACACCCGACAAAGTCCCAACGTATCCCTG 1095
Db 42 CGACCCGACGCTAGGACATATGATGCTCTCGTAGACAAATCGTCCATCTCTTC 101
QY 1096 ACGCTGATCGGACCATCTACAGCGTTCATGCTGAGTTCTTGGGCGAAGTGGGACTC 1155
Db 102 GGAGCGAGTTTCAATCCCTCGACGATATATGATTAGCTCTGTCGGGCAAGTGTCAACTGC 161
QY 1156 TGGATTACGACTTGGGCTCGGACTGGTAAAGCCGAGACTGTGAGAGCGCAATCTTT 1215
Db 162 TATGAATTAGACTTCGGATTGCGGCTTGGAAAGCCGGAGGCTGTGCGACCGCAATTC 221
QY 1216 GAGCTCTGTGAGAGTTGATGTACTTTATGCCAAGAGCCTGATGCGGAGTTCTGTGCG 1275
Db 222 ACTCGGTTGAGGTTGATTTATTTATTCATGCCAAGAGGCTGTGTCGAGATTGCTGTT 281
QY 1276 GCGCTTTCTTGAGGATAGGATATGAGCCGATTGAAGCGGATAGAGTGGACCAAG 1335
Db 282 GCTGCTCGTTACAGGAGGAGATATGCGCGGTTTGGCGGATGAAGAGTTTACGAAG 341
QY 1336 TATCGGAGTACGTTGGTTAG 1356
Db 342 TTTGGCAATATATCCCTTAG 362
RESULT 10
ADA71938
ID ADA71938 standard; DNA; 2000 BP.
XX
XX ADA71938;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Rice gene, SEQ ID 5263.
DE
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW

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KW gene; ds.
XX
OS Oryza sativa.
XX
XX WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
DR
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 27; SEQ ID NO 5263; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
XX Sequence 2000 BP; 336 A; 285 C; 284 G; 363 T; 0 U; 752 Other;
SQ
Query Match 3.7%; Score 50.4; DB 8; Length 2000;
Best Local Similarity 9.9%; Pred. No. 0.00013;
Matches 62; Conservative 292; Mismatches 268; Indels 6; Gaps 2;
QY 725 CAGAGCTAAGATCTCTGCTACCAAGACTCTTGACGATCAACAAGTCTGTCGACTG 784
Db 29 CARMGSSRMKMGMSKRYKSCGCKMTTRKSKWYSASSASGRGTGSKWSSGYSYK 88
QY 785 ACGATGCTCTTCGCGGTTCACTCGAAATCGGCTCTCGGTCGCTCGGAAAGATCG 844
Db 89 GKKRYKSKRWGRGRGRMRSRMRWGRYPRCARSGRMAGSGRMGKSRMSYMMWC 148
QY 845 ATGGCTCTGCACCTACCGAGTTCTCCGCTG--CTTTGATGCTCGACGGCAATGGTGT 902
Db 149 YARGCGSKRKXKSGSGWGTCTCRRGARGSGWSGAKYKSGMSKRMWMSCGRSGCRR 208
QY 903 CTCGAACAACACTACCAGGCTTCTTCAAACACTACCTACCACTACCATCGGCA 962
Db 209 SAYSYRYGTSRYKTYKMTYYASRCRMAYMTTYSWACSSYTWCRSKRSMWMMRK 268
QY 963 AATCGCCAACGAGTCACTCGCGCAACAGCATCATCGCTTCGTTGAGAACTCGACCCCG 1022
Db 269 MWRSSRYGHSYKXWMCCTAYKYSYRWYVGRGWRGATRYWGRGYMSRMAMMYKK 328
QY 1023 GAGCATGCCCGAGCGAACAAGAGGTTCTCGGAGCTCTCGGACACACACCCCGACAAGTC 1082
Db 329 MYWRYGKMGKRWAGRMMSKRWKACCYMWRMWRMTTRRRWAKSKSRTRRRKKR 388
QY 1083 CAACGTATCCCTGACGCTGATGCGGACCCATCTACACGCTCATGCTCAGTTCTTGGGC 1142
Db 389 KWCRRKRYKMRGYSRMSCKRMRWKRGRGAWKRCRGMTCRMSYGMWRKWSK 448
QY 1143 CAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTGAG 1202

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449 RMASKYK-----WMSRMYRWKKKCSRTTMMGKTGGHMTGWRCRYKKRSQMKKCRRRR 504

1203 ACGGCCAATCTTTGAGCCTGTGAGACCTTCATGTACTTTATGCACCAGAAGCCCTGATGG 1262  
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :  
505 WGRMYRMWRKYMSARYTWRYCARKKYSYAARKARCWYRGKYIWAGMMWKYKEMYM 564

1263 CGAGTTCTTGTCGGCGCGCTTCTCTGAGGGATGAGGATATGACCGATTGAAGCGCGGATAA 1322  
: : : : : : : : : : : : : : : : | : : : : : : | : : : : : : | : : : : : :  
565 YKMWWYKRKYSCSWYCKMSYVASCMSAKKAGAKMKCKRSKMSAWSKMSRSSRKCKCA 624

1323 GGAGTGACCAAGTATGCGCAGTAGCTT' 1350  
: : : : : : | : : : : : : | : : : : : : | : : : : : : | : : : : : :  
625 SKRSSAKRYAMMGMTSGSRMSRWKSYT 652

RESULT 11  
ADA71938/c  
ID ADA71938 standard; DNA; 2000 BP.  
XX  
XX ADA71938;  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 5263.  
XX Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
XX Oryza sativa.  
OS  
XX WO2003000898-A1.  
PN  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
PR  
XX 22-JUN-2001; 2001WO-IB001105.  
PR  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
PI  
XX WPI; 2003-175290/17.  
DR  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
XX Claim 27; SEQ ID NO 5263; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX  
SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 3.0%; Score 40.2; DB 8; Length 2000;  
Best Local Similarity 9.2%; Pred. No. 0.22;  
Matches 55; Conservative 287; Mismatches 255; Indels 4; Gaps 3;

QY 165 GGTGCGAGCGCAGGTCAAAGCGGAGCATTAAGCGAGGAAACAAGGAATCTCTTTAT 224  
:: :::::: ::::: : : : : | : : : : : : | : : : : : : | : : : : : :  
DB 706 KRSYRYYRWYTKRGWTYRVYRWSCRWTRARSKRKWKAGASMKSCWMYWRGARSMWY 647

Qy	225	CGTCCCTTTTGAGGAGCTTCTCGTGTGTGTAGTGAAGAAGACCTCCGCGCATGATCCTTCAGC	28
Db	646	SYKSAKCKKRYM--TSSYNSTGMYGMYSSYKSWTSWTSKMSYMGKMTCTWYTSKMS	589
Qy	285	GCCACGATCAGGGTATGAGAAAGG-CGGGATACCCCTATGGCGATCTTTTGACGAGAACA	343
Db	588	TRSKWGRWSGSRMYMWWKMRKRYMYRMKWKCTWRRCMKCYRWGYTWTWYTSRSMY	529
Qy	344	TCATCGCGCCAGGAAGACGTTTACCTATTTGGACCTCGTATCTGGTCCGACGACCCAAAGC	403
Db	528	TGRYKARYTSKERYMYKYRYKYCYWYYYGYMYMKSYYMYRYGKCKKCCYAMCWKAAYS	469
Qy	404	CTGTAACTTATTCAGCTCAACTTCATCAAGGGCGACTCATCTCTCACTGTCAACGGAC	463
Db	468	GMMWTYIRKYSKWRMRSTKYMYMWMYKCRSMKYGAKGCGCKRMWTCYSGYMKWYTYMG	409
Qy	464	AGCACGGTCTATGGATATGTTAGGCCCAAGATGCGGTGATCCGCTACTCTCCAAGCGT	523
Db	408	SVKSRCKYKMYMYMKGMMYMYSAVSSMTWYTYAKTWKYWRGTMSWYKSYK	349
Qy	524	GCGCTAAACGACCATTACACCAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGA	583
Db	348	KKYCYWCMYKCMR-CYWRKMRKKTYSKRCYCRVATCYWCCCYRKGWYRSRSMR	290
Qy	584	TAGTTCCTTACCTGAAAACATATACGATTGCGCCGAGGTAGATCATCATGATGTCTAAG	643
Db	289	TAGKWRMSRWSRCSYSWYKMYKMWKKSYYMSYGNARSSGTWRSAAKRTYKGYSTR	230
Qy	644	CTGATGTAGCTGGTGGTGAACGCTGTTCTCAGCCGGTCAGTGCAAGCTGGGCGTCTTCA	703
Db	229	RAKMRACRMYSACRYRSTSYCGCSYCGSKWYMSKSGSMRMTCSMCOCYTCYG	1700
Qy	704	CATTACGCCCCAAGCCATGTACAGAGCTCAAGGATGCTGTACCAAGACTCTTGAAGCAT	763
Db	169	AMCNSCCSMYMGSGCYTRGNWRKRSKYSMCKKYCSCCTKCSYTGYYRYCKWYKYS	110
Qy	764	C 764	
Db	109	Y 109	
RESULT 12			
ADI81367			
ADI81367 standard; DNA; 663 BP.			
XX	AC	ADI81367;	
XX	DT	22-APR-2004 (first entry)	
XX	DE	M. tuberculosis VNTR locus Mtb-v18 nucleotide sequence.	
XX	KW	valuable number tandem repeat; VNTR; Mycobacterium tuberculosis;	
XX	KW	detection; tuberculosis; gene; ds.	
XX	OS	Mycobacterium tuberculosis.	
XX	BN	W02004009837-A2.	
XX	PD	29-JAN-2004.	
XX	PF	21-JUL-2003; 2003MO-US022950.	
XX	XX	19-JUL-2002; 2002US-0397224P.	
XX	XX	(UYAR-) UNIV ARIZONA.	
XX	PA	(KEIM/) KEIM P S.	
XX	PA	(SCHU/) SCHUPP J M.	
XX	PA	(SPUR/) SPURGIESZ R S.	
XX	XX	Keim PS, Schupp JM, Spurgiesz RS;	
XX	PI	WPI; 2004-123400/12.	
XX	DR		
XX	XX		

PT New isolated nucleic acid, useful for detecting Mycobacterium  
PT tuberculosis species in assays employing probes, including a  
XX nanodetection device.

PS Example 8; Page 24-25; 44pp; English.

XX  
CC The present invention describes an isolated nucleic acid (1) comprising  
CC at least 12 consecutive nucleotides of a nucleotide sequence selected  
CC from the 18 sequences of SEQ ID NO: 1-18 (AD181342 to AD181359) or the  
CC complementary sequences of SEQ ID NO: 1-18. Also described: (1) a pair of  
CC forward and reverse primers for amplification of valuable number tandem  
CC repeats (VNTR) located in DNA isolated from Mycobacterium tuberculosis  
CC species, where the pair is selected from SEQ ID NO: 1 and 2; SEQ ID NO: 3  
CC and 4; SEQ ID NO: 5 and 6; SEQ ID NO: 7 and 8; SEQ ID NO: 9 and 10; SEQ  
CC ID NO: 11 and 12; SEQ ID NO: 13 and 14; SEQ ID NO: 15 and 16 or SEQ ID  
CC NO: 17 and 18; (2) a method for detecting a M. tuberculosis species; (3)  
CC a kit for the detection of a M. tuberculosis species comprising: (a) the  
CC pair of forward and reverse primers; (b) nucleic acids having an  
CC observable marker; (c) a transcriptase; and (d) buffers and salts  
CC suitable for causing polymerisation of VNTR in DNA from the M.  
CC tuberculosis species in a polymerase chain reaction (PCR); and (4) a  
CC method of sub-typing a M. tuberculosis strain. The pair of forward and  
CC reverse primers are useful as PCR primers in the detection of M.  
CC tuberculosis species. The kit is useful for multiplexing DNA from a M.  
CC tuberculosis species, where the kit comprises mixtures of the pair of  
CC forward and reverse primers for use in a multiplex instrument. The  
CC nucleic acid is useful for detecting M. tuberculosis species in assays  
CC employing probes, including a nanodetection device. The sub-typing scheme  
CC is useful for the epidemiological study of M. tuberculosis and may be  
CC applied to the local detection of the pathological causative agent of  
CC tuberculosis. The present sequence represents a M. tuberculosis VNTR  
CC locus Mtb-v18 nucleotide sequence, which is used in an example from the  
XX present invention.

SQ Sequence 663 BP; 135 A; 208 C; 213 G; 107 T; 0 U; 0 Other;

Query Match 2.9%; Score 39.8; DB 12; Length 663;  
Best Local Similarity 49.8%; Pred. No. 0.16;  
Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;  
QY 956 TCGGCGAATGCCAACGAGTCACTCGCGCAACAGCATCAGCCCTTCGTTGAGAACTCG 1015  
DB 433 TCGAGAGGTTTCGCGCGCCGCTCGAGAGCCAGCCGCAATCGGCTACCGGATATCC 492  
QY 1016 ACCCGCGAGCATCGCGCAACAGAGGTCTCGCGACGTACCTGCAACAACACCCCG 1075  
DB 493 AGCCACAGCATCCGCAACTCGAGATGTTCTGCGCCCGCACTGCGGAGGAGCTCG 552  
QY 1076 ACAAGTCCAACTATCCCTGAGCGGTGATGCGGACCCATCTACCGCGTCTGCTGAGTT 1135  
DB 553 ACCGGCTTACCTGCGTTCAACGAGGAGCGCGTGCCTCGGACGCCGAGTTGCGCATTG 612  
QY 1136 CTGGGCGGAGTGGGACTCTGG 1158  
DB 613 CCCAGGCACAGCTGTCGGCTGG 635

## RESULT 13

AAI99682\_42  
Continuation (43 of 45) of AAI99682 from base 4200001 (Mycobacterium tuberculosis strain  
WP Sequence split into 45 fragments LOCUS AAI99682 Accession AAI99682

WP	Fragment Name	Begin	End
WP	AAI99682_00	1	110000
WP	AAI99682_01	100001	210000
WP	AAI99682_02	200001	310000
WP	AAI99682_03	300001	410000
WP	AAI99682_04	400001	510000
WP	AAI99682_05	500001	610000
WP	AAI99682_06	600001	710000
WP	AAI99682_07	700001	810000
WP	AAI99682_08	800001	910000
WP	AAI99682_09	900001	1010000
WP	AAI99682_10	1000001	1110000

WP	AAI99682_11	1100001	1210000
WP	AAI99682_12	1200001	1310000
WP	AAI99682_13	1300001	1410000
WP	AAI99682_14	1400001	1510000
WP	AAI99682_15	1500001	1610000
WP	AAI99682_16	1600001	1710000
WP	AAI99682_17	1700001	1810000
WP	AAI99682_18	1800001	1910000
WP	AAI99682_19	1900001	2010000
WP	AAI99682_20	2000001	2110000
WP	AAI99682_21	2100001	2210000
WP	AAI99682_22	2200001	2310000
WP	AAI99682_23	2300001	2410000
WP	AAI99682_24	2400001	2510000
WP	AAI99682_25	2500001	2610000
WP	AAI99682_26	2600001	2710000
WP	AAI99682_27	2700001	2810000
WP	AAI99682_28	2800001	2910000
WP	AAI99682_29	2900001	3010000
WP	AAI99682_30	3000001	3110000
WP	AAI99682_31	3100001	3210000
WP	AAI99682_32	3200001	3310000
WP	AAI99682_33	3300001	3410000
WP	AAI99682_34	3400001	3510000
WP	AAI99682_35	3500001	3610000
WP	AAI99682_36	3600001	3710000
WP	AAI99682_37	3700001	3810000
WP	AAI99682_38	3800001	3910000
WP	AAI99682_39	3900001	4010000
WP	AAI99682_40	4000001	4110000
WP	AAI99682_41	4100001	4210000
WP	AAI99682_42	4200001	4310000
WP	AAI99682_43	4300001	4410000
WP	AAI99682_44	4400001	4411529

Query Match 2.9%;

Best Local Similarity 49.8%; Score 39.8; DB 4; Length 110000;

Pred. No. 2.4;

Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY	956 TCGGCGAATGCCAACGAGTCACTCGCGCAACAGCATCAGCCCTTCGTTGAGAACTCG 1015
DB	27170 TCGAGAGGTTTCGCGCGCCGCTCGAGAGCCAGCCGCAATCGGCTACCGGATATCC 27229
QY	1016 ACCCGCGAGCATCGCGCAACAGAGGTCTCGCGACGTACCTGCAACAACACCCCG 1075
DB	27230 AGCCACAGCATCCGCAACTCGAAGATGTTCTGCGCCCGCACTGCGGAGGAGCTCG 27289
QY	1076 ACAAGTCCAACTATCCCTGAGCGGTGATGCGGACCCATCTACCGCGTCTGCTGAGTT 1135
DB	27290 ACCGGCTTACCTGCGTTCAACGAGGAGCGCGTGCCTCGGACGCCGAGTTGCGCATTG 27349
QY	1136 CTGGGCGGAGTGGGACTCTGG 1158
DB	27350 CCCAGGCACAGCTGTCGGCTGG 27372

## RESULT 14

AAI99683\_42

Continuation (43 of 44) of AAI99683 from base 4200001 (Mycobacterium tuberculosis strain  
WP Sequence split into 44 fragments LOCUS AAI99683 Accession AAI99683

WP	Fragment Name	Begin	End
WP	AAI99683_00	1	110000
WP	AAI99683_01	100001	210000
WP	AAI99683_02	200001	310000
WP	AAI99683_03	300001	410000
WP	AAI99683_04	400001	510000
WP	AAI99683_05	500001	610000
WP	AAI99683_06	600001	710000
WP	AAI99683_07	700001	810000
WP	AAI99683_08	800001	910000
WP	AAI99683_09	900001	1010000
WP	AAI99683_10	1000001	1110000
WP	AAI99683_11	1100001	1210000

WP	AAI99683_12	1200001	1310000
WP	AAI99683_13	1400001	1410000
WP	AAI99683_14	1400001	1510000
WP	AAI99683_15	1500001	1610000
WP	AAI99683_16	1500001	1710000
WP	AAI99683_17	1700001	1810000
WP	AAI99683_18	1800001	1910000
WP	AAI99683_19	1900001	2010000
WP	AAI99683_20	2000001	2110000
WP	AAI99683_21	2100001	2210000
WP	AAI99683_22	2200001	2310000
WP	AAI99683_23	2300001	2410000
WP	AAI99683_24	2400001	2510000
WP	AAI99683_25	2500001	2610000
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WP	AAI99683_30	3000001	3110000
WP	AAI99683_31	3100001	3210000
WP	AAI99683_32	3200001	3310000
WP	AAI99683_33	3300001	3410000
WP	AAI99683_34	3400001	3510000
WP	AAI99683_35	3500001	3610000
WP	AAI99683_36	3600001	3710000
WP	AAI99683_37	3700001	3810000
WP	AAI99683_38	3800001	3910000
WP	AAI99683_39	3900001	4010000
WP	AAI99683_40	4000001	4110000
WP	AAI99683_41	4100001	4210000
WP	AAI99683_42	4200001	4310000
WP	AAI99683_43	4300001	4403765

Query Match 2.9%; Score 39.8; DB 4; Length 110000;

Best Local Similarity 49.8%; Pred. No. 2.4; Indels 0; Gaps 0;

Matches 101; Conservative 0; Mismatches 102;

Qy	956	TCGGCGAAATCGGCACAGAGTCACTCGGGCGCAACAGCATCAGCGCTTCGTTCCAGAACTCG	1015
Db	19416	TCGAGGAGGTTTCGGCGGCCCACTCGACGAGCGCAGCGCATCGGCTACGCGATATCC	19475
Qy	1016	ACCCGCGGAGCATTGCGCAGCGAACAAGAGGTTCTCGGACGTTACTGCACAACAACCCCG	1075
Db	19476	ACGCCACCACTCCCGCAACTCGAAGATGGTCTGGCCCGGAACTCGCGGAGGACTCG	19535
Qy	1076	ACAAGTCCACAGTATCCCTGACGGCTGATCGGACCCATCTACGAGCGTCATGCTGAGTT	1135
Db	19536	ACCGGCTTACCTTGCCTTCAACGAGGACCGCGTGCCTTCGACGCCGAGTTGCGCATTTG	19595
Qy	1136	CTTGGGCGCAAGTGGGACTCTGG	1158
Db	19596	CCCAGGCACAGTGTGCTGGCTGG	19618

RESULT 15

AAAT37310

ID AAT37310 standard; cDNA to mRNA; 1605 BP.

XX AAT37310;

XX

16-OCT-2003 (revised)

DT 06-FEB-1997 (first entry)

XX

XX

DE Aromatic acyl transferase coding sequence.

XX Aromatic acyl transferase; transformation; anthocyanin pigment; plants;

KW acylation; colour; tone; colouration; colour change; Gentiana triflora;

KW Petunia hybrida; Perilla ocimoides; Senecio cruentus;

KW Lavandula angustifolia; ds.

XX

OS Petunia x hybrida; (Clone pPAT48).

XX

FH Key Location/Qualifiers

[illegible]

Search completed: January 23, 2005, 14:47:30  
Job time : 737 secs

Aromatic acyl transferase coding sequence.

Aromatic acyl transferase; transformation; anthocyanin pigment; plants; KW  
 acylation; colour; tone; colouration; colour change; *Gentiana triflora*; KW  
 Petunia hybrida; *Perilla* oimoides; *Scenecio* cruentus; KW  
 Lavandula angustifolia; ds. KW

XX OS Petunia x hybrida; (Clone pPAT48).

XX	Key	Location/Qualifiers
FH		



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 21:45:08 ; Search time 6029 Seconds  
(without alignments)  
10636.064 Million cell updates/sec

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Perfect score: 1356  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1356	100.0	1356	6	AR193433 Sequence
3	1356	100.0	1356	6	AR430218 Sequence
4	1340	98.8	1605	6	E31785 Trichothec
5	1340	98.8	1605	8	AB000874
6	1340	98.8	3003	8	AB009607 Gibberell
7	1340	98.8	8646	8	AB011417 Gibberell
8	1334	98.4	1336	8	AF212605 Gibberell
9	1334	98.4	1336	8	AF212608 Gibberell
10	1330.8	98.1	1336	8	AF212603 Gibberell
11	1330.8	98.1	1336	8	AF212606 Gibberell
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25	1318	97.2	1336	8	AF212595 Gibberell
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28	1318	97.2	1336	8	AF212598 Gibberell
29	1318	97.2	1336	8	AF212599 Gibberell
30	1318	97.2	1336	8	AF212600 Gibberell
31	1316.4	97.1	1336	8	AF212588 Gibberell
32	1314.8	97.0	1326	8	AY452813 Fusarium
33	1314.8	97.0	1326	8	AY452814 Fusarium
34	1314.8	97.0	1336	8	AF212589 Gibberell
35	1310	96.6	1326	8	AY452810 Fusarium
36	1310	96.6	1326	8	AY452811 Fusarium
37	1310	96.6	1326	8	AY452812 Fusarium
38	1304.4	96.2	1322	8	AY222842 Gibberell
39	1304.4	96.2	1322	8	AY225882 Gibberell
40	1303.6	96.1	1336	8	AF212590 Gibberell
41	1303.6	96.1	1336	8	AF212591 Gibberell
42	1303.6	96.1	1336	8	AF212592 Gibberell
43	1303.6	96.1	1336	8	AF212593 Gibberell
44	1287.6	95.0	1336	8	AF212614 Fusarium
45	1284.4	94.7	1336	8	AF212612 Fusarium

ALIGNMENTS

RESULT 1  
BD247864  
LOCUS  
DEFINITION Transgenic plant and methods.  
ACCESSION BD247864  
VERSION BD247864.1 GI:33057634  
KEYWORDS JP 2002540787-A/4.  
SOURCE Gibberella zeae  
ORGANISM Gibberella zeae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
REFERENCE 1 (bases 1 to 1356)  
Hohn,T.M., Peters,C., Salmeron,J.M., Janet, Reed,N. and Dawson,J.L.  
AUTHORS Hohn,T.M., Peters,C., Salmeron,J.M., Janet, Reed,N. and Dawson,J.L.  
TITLE Transgenic plant and methods  
JOURNAL Patent: JP 2002540787-A 4 03-DEC-2002;  
SYNGENTA PARTICIPATIONS AG  
COMMENT OS Fusarium graminearum  
PN JP 2002540787-A/4  
PD 03-DEC-2002  
PF 29-MAR-2000 JP 2000609553  
PR 31-MAR-1999 US 09/282995,11-FEB-2000 US 09/502852 PI  
THOMAS M HOHN,CHERYL PETERS,JOHN MANUEL SALMERON,JANET PI N  
REED,JOHN L DAWSON  
PC C12N15/09,A01H5/00,C12N1/15,C12N5/10//C12N1/15,C12R1:645), PC  
(C12N5/10,C12R1:91),C12N15/00,C12N5/00,C12N5/00,C12R1:91) CC  
Transgenic plant and methods  
FH Key Location/Qualifiers  
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/mol\_type='genomic DNA'  
/db\_xref='taxon:5518'

Query Match 100.0%; Score 1356; DB 6; Length 1356;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCTTTCAAGTACAGCTCGACCCCTCGGCAGCTACCGGCTCTTCGATCTAC 60  
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Qy      61  ACCAAATCAGTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTCTCAGC  120
Db      61  ACCAAATCAGTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTCTCAGC  120
Qy     121  ACTTCGACGAAGTCTTAAGCGCTTCTCCGAAGCGCTCCCATGGTGCAGGCCAGGTC  180
Db     121  ACTTCGACGAAGTCTTAAGCGCTTCTCCGAAGCGCTCCCATGGTGCAGGCCAGGTC  180
Qy     181  AAAGCCGAGGCGATTAAGCGAGGGAACAACAGGAACCTCTCTTTATCGTCCCTTTGAGAC  240
Db     181  AAAGCCGAGGCGATTAAGCGAGGGAACAACAGGAACCTCTCTTTATCGTCCCTTTGAGAC  240
Qy     241  GTTCTCGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCAGGGT  300
Db     241  GTTCTCGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCAGGGT  300
Qy     301  ATGAGAAAGCGGGATACCTATGGCGATGTTTGAAGGAACATCATCGGCCAAGGAAG  360
Db     301  ATGAGAAAGCGGGATACCTATGGCGATGTTTGAAGGAACATCATCGGCCAAGGAAG  360
Qy     361  ACCTTACCTATTGACCTGCTGCTCCGACGACCCAAAGCCTGTAAATCTATTGCGAG  420
Db     361  ACCTTACCTATTGACCTGCTGCTCCGACGACCCAAAGCCTGTAAATCTATTGCGAG  420
Qy     421  CTCAACTTATCAAGGCGGACTCATCTCACTGTCACGAGCAGCACCGTCTATGGAT  480
Db     421  CTCAACTTATCAAGGCGGACTCATCTCACTGTCACGAGCAGCACCGTCTATGGAT  480
Qy     481  ATGGTAGGCCAAGATCGGCTGATCCCTCTACTCTCAAGCGCTGCGGTAAACCACTTC  540
Db     481  ATGGTAGGCCAAGATCGGCTGATCCCTCTACTCTCAAGCGCTGCGGTAAACCACTTC  540
Qy     541  ACCGAAGAGGAATAGACGGCCATGAACCTGATCGAAGCAGATGTTCTTACCTTGA  600
Db     541  ACCGAAGAGGAATAGACGGCCATGAACCTGATCGAAGCAGATGTTCTTACCTTGA  600
Qy     601  AACTATACGATTCGCCCGAGGTAGATCATCATGTTCAAGCTCATGTAGCTGTGTGT  660
Db     601  AACTATACGATTCGCCCGAGGTAGATCATCATGTTCAAGCTCATGTAGCTGTGTGT  660
Qy     661  GAGCTGTTCTACGCGCGTCACTGCAAGCTGCGGCTTCTTCAATTCAGCCCAAGGCC  720
Db     661  GAGCTGTTCTACGCGCGTCACTGCAAGCTGCGGCTTCTTCAATTCAGCCCAAGGCC  720
Qy     721  ATGTACAGCTCAAGGATGCTGTACCAAGACTTTGACGCAATCAACAAAGTTCTGTG  780
Db     721  ATGTACAGCTCAAGGATGCTGTACCAAGACTTTGACGCAATCAACAAAGTTCTGTG  780
Qy     781  ACTGACGATGCTTTTCGGGCTTCACTCTGGAATCGGCTCTCGCGTGTGCTCTGAAAGA  840
Db     781  ACTGACGATGCTTTTCGGGCTTCACTCTGGAATCGGCTCTCGCGTGTGCTCTGAAAGA  840
Qy     841  ATCGATGCTCTGACCTACCGAGTTCCTGCGTCTGTGATGCTGACCGCAATGGGT  900
Db     841  ATCGATGCTCTGACCTACCGAGTTCCTGCGTCTGTGATGCTGACCGCAATGGGT  900
Qy     901  GTCTCGAAACAACTACCCAGGCTTCTTCAAAATGACCTACCAACTCGACCATCGGC  960
Db     901  GTCTCGAAACAACTACCCAGGCTTCTTCAAAATGACCTACCAACTCGACCATCGGC  960
Qy     961  GAAATCGCAACGATGCTCTGCGCGCAACAGCATCAAGCTTCTGTTTCAAGAACTCGA  1020
Db     961  GAAATCGCAACGATGCTCTGCGCGCAACAGCATCAAGCTTCTGTTTCAAGAACTCGA  1020
Qy    1021  GCGAGCTATGCGCAACGAAGAGTCTGCGAGCTGCTGACGATCACTGCAACCAACCCG  1080
Db    1021  GCGAGCTATGCGCAACGAAGAGTCTGCGAGCTGCTGACGATCACTGCAACCAACCCG  1080
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Qy     1141  GCCAAGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG  1200
Db     1141  GCCAAGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG  1200
Qy     1201  AGACGGCCAAATCTTTGAGCCCTGTTGAGAGCTTGTATGTAATGATGATGATGATGAT  1260
Db     1201  AGACGGCCAAATCTTTGAGCCCTGTTGAGAGCTTGTATGTAATGATGATGATGATGAT  1260
Qy     1261  GGCGAGTTCGTGCGGCGCTTCTCTGAGGATGAGGATGAGACCGATGGAAGCGGAT  1320
Db     1261  GGCGAGTTCGTGCGGCGCTTCTCTGAGGATGAGGATGAGACCGATGGAAGCGGAT  1320
Qy     1321  AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG  1356
Db     1321  AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG  1356
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RESULT 2
AR193433 1356 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5 from patent US 6346655.
DEFINITION
ACCESSION AR193433
VERSION AR193433.1 GI:20239398
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.
TITLE Trichothecene-Resistant transgenic plants
JOURNAL Patent: US 6346655-A 5 12-FEB-2002;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION	AR430218			
VERSION	AR430218.1	GI:40190948		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1356)			

AUTHORS	Hohn,T.M., Peters,C. and Salmerton,J.									
TITLE	Trichothecene-resistant transgenic plants									
JOURNAL	Patent: US 6646184-A 5 11-NOV-2003;									
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 VERSION E31785.1 GI:13018619  
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 ORGANISM Gibberella zeae  
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 1 (bases 1 to 1605)  
 Isamu, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.  
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 PD 02-FEB-2000  
 PF 15-JUL-1998 JP 1998200280  
 PR ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI KOSHINO, PI KATSUMI YONEYAMA  
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 ACCESSION AB000874  
 VERSION AB000874.1 GI:2804249  
 KEYWORDS trichothecene 3-O-acetyltransferase.  
 SOURCE Gibberella zeae  
 ORGANISM Gibberella zeae  
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 Kimura, M., Kaneko, I., Komiyama, M., Takatsuki, A., Koshino, H., Yoneyama, K. and Yameguchi, I.  
 Trichothecene 3-O-acetyltransferase protects both the producing organism and transformed yeast from related mycotoxins. Cloning and characterization of Tril01  
 J. Biol. Chem. 273 (3), 1654-1661 (1998)  
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 2 (bases 1 to 1605)  
 Kimura, M.  
 Direct Submission  
 Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical and Chemical Research (RIKEN), Microbial Toxicology Laboratory, Hiroshima 2-1, Wako, Saitama 351-01, Japan  
 (E-mail: mkimura@postman.riken.go.jp, Tel:81-048-467-9518, Fax:81-048-462-4676)

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ORIGIN

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LOCUS	AB011417		PLN 05-FEB-1999
DEFINITION	Gibberella zeae genes for trichothecene 3-O-acetyltransferase, UTP-ammonia ligase and phosphate permease, complete cds.		
ACCESSION	AB011417		
VERSION	AB011417.1	GI:3724288	
KEYWORDS	phosphate permease; UTP-ammonia ligase; Tri101; trichothecene 3-O-acetyltransferase.		
SOURCE	Gibberella zeae		
ORGANISM	Gibberella zeae		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.		
AUTHORS	Kimura, M., Matsumoto, G., Shingu, Y., Yoneyama, K. and Yamaguchi, I.		
TITLE	The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the region around Tri101 and characterization of its homologue from Fusicarpa sporotrichioides		
JOURNAL	FEMS Lett. 435 (2-3), 163-168 (1998)		
MEDLINE	98433864		
PUBMED	9762900		
REFERENCE	2 (bases 1 to 8646)		
AUTHORS	Kimura, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-FEB-1998) Makoto Kimura, The Institute of Physical and Chemical Research (RIKEN), Microbial Toxicology Laboratory; Hiroseawa 2-1, Wako, Saitama 351-0198, Japan		
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DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212605
VERSION AF212605.1 GI:12003706
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SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. H.
TITLE Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
PROC. NATL. ACAD. SCI. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL 20345085
MEDLINE 10869425
PubMed 10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS O'Donnell, K.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
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LOCUS Gibberella zeae strain NRRL29169 trichothecene

DEFINITION 3-O-acetyltransferase, partial cds.

ACCESSION AF212608

VERSION AF212608.1 GI:12003712

KEYWORDS

SOURCE Gibberella zeae

ORGANISM Gibberella zeae

REFERENCE 1 (bases 1 to 1336)

AUTHORS O'Donnell K., Kistler, H. C., Tacke, B. K. and Casper, H. H.

TITLE Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)

MEDLINE 20345085

PUBMED 10869425

REFERENCE 2 (bases 1 to 1336)

AUTHORS O'Donnell, K.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA

FEATURES

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LOCUS Gibberella zeae strain NRRL6394 trichothecene  
DEFINITION 3-O-acetyltransferase, partial cds.  
ACCESSION AF212603  
VERSION AF212603.1 GI:12003702  
KEYWORDS  
SOURCE Gibberella zeae  
ORGANISM Gibberella zeae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 1336)  
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.  
Gene genealogies reveal global phylogeographic structure and  
reproductive isolation among lineages of *Fusarium graminearum*, the  
fungus causing wheat scab  
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)

JOURNAL 20345085  
MEDLINE 10869425  
PUBMED  
REFERENCE 2 (bases 1 to 1336)  
O'Donnell, K.  
Direct Submission  
Submitted (08-DEC-1999) Microbial Properties Research,  
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA

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DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212606
VERSION AF212606.1 GI:12003708
KEYWORDS Gibberella zeae
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
TITLE Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
PUBMED 10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS O'Donnell, K.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.		
	Gene genealogies reveal global phylogeographic structure and		
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	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)		
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REFERENCE	O'Donnell, K.		
AUTHORS	Direct Submission		
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JOURNAL	NCAUR-ARS-5094, 1815 N. University St., Peoria, IL 61604, USA		
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DB 1323 AAGGAGTGGACCAA 1336  
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LOCUS  
DEFINITION  
Gibberella zeae strain NRRRL5883 trichothecene  
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ACCESSION  
AF212602  
VERSION  
AF212602.1 GI:12003700  
KEYWORDS  
Gibberella zeae  
ORGANISM  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
REFERENCE  
1. (bases 1 to 1336)  
O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. H.  
Gene genealogies reveal global phylogeographic structure and  
reproductive isolation among lineages of *Fusarium graminearum*, the  
fungus causing wheat scab  
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)  
JOURNAL  
MEDLINE  
20345085  
PUBMED  
10869425  
REFERENCE  
2. (bases 1 to 1336)  
O'Donnell, K.  
Direct Submission  
TITLE  
Submitted (08-DEC-1999) Microbial Properties Research,  
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA  
JOURNAL  
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ORIGIN

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DEFINITION	Gibberella zeae strain NRRL1338; trichothecene 3-O-acetyltransferase, partial cds.		PLN 26-JUN-2001
ACCESSION	AF212604		
VERSION	AF212604.1	GI:12003704	
KEYWORDS			
SOURCE	Gibberella zeae		
ORGANISM	Gibberella zeae		
REFERENCE	1 (bases 1 to 1336)		
AUTHORS	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.		
TITLE	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (14), 7905-7910 (2000)	
MEDLINE	20345085		
PUBMED	10869425		
REFERENCE	2 (bases 1 to 1336)		
AUTHORS	O'Donnell, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA		
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AY452807  
VERSION  
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KEYWORDS  
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
REFERENCE  
1 (bases 1 to 1329)  
O'Donnell K., Ward, T.J., Geiser, D.M., Corby Kistler, H. and Aoki, T.  
Genetical concordance between the mating type locus and seven  
other nuclear genes supports formal recognition of nine  
phylogenetically distinct species within the Fusarium graminearum  
clade  
Fungal Genet. Biol. 41 (6), 600-623 (2004)  
PUBMED  
15121083  
REFERENCE  
2 (bases 1 to 1329)  
O'Donnell K.  
Direct Submission  
Submitted (29-OCT-2003) Microbial Genomics, USDA, ARS, 1815 N.  
University St., Peoria, IL 61604, USA  
JOURNAL  
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Wed Jan 26 11:53:55 2005

us-10-614-954-5.rge

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 23, 2005, 17:51:03 ; Search time 102 Seconds  
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Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2314	99.1	451	2	O42692 gibberella
2	2296	98.4	444	2	Q9HDE2
3	2291	98.2	444	2	Q9HDE5
4	2287	98.0	442	2	O6JTY2
5	2286	97.9	444	2	Q9HF40
6	2277	97.6	444	2	Q9HDF3
7	2276	97.5	444	2	Q9HDE8
8	2273	97.4	444	2	Q9HFA2
9	2273	97.4	444	2	Q9HFA1
10	2272	97.3	444	2	Q9HDN2
11	2271	97.3	444	2	Q9HDI5
12	2265	97.0	444	2	Q9HDE0
13	2262	96.9	441	2	O6JTX6
14	2257	96.7	444	2	Q9HF38
15	2255	96.6	444	2	Q9HF39
16	2254	96.6	441	2	O6JTX9
17	2247	96.3	444	2	Q9HDL5
18	2244	96.1	440	2	Q86232
19	2236	95.8	444	2	Q9HDM1
20	2196	94.1	444	2	Q9HDM0
21	2059	88.2	418	2	O6JTY1
22	1860.5	79.7	459	2	Q96VQ8
23	1857.5	79.6	459	2	Q94197
24	1828.5	78.3	459	2	O74644
25	1582	67.8	453	2	Q862D5
26	1512	64.8	454	2	Q862D2
27	1478	63.3	454	2	O862E4
28	962.5	41.2	474	2	O12226
29	945	40.5	454	2	O6BSF1
30	878.5	37.6	469	2	O6C6T8
31	253.5	10.9	493	2	Q86265

32 178 7.6 442 2 Q6K638  
33 178 7.6 442 2 BAD19683  
34 175 7.5 439 2 Q84QG6  
35 175 7.5 464 2 Q6ZCD2  
36 175 7.5 464 2 BAD09504  
37 173.5 7.4 430 2 Q7XPK8  
38 172.5 7.4 445 2 Q6YYV8  
39 172.5 7.4 445 2 BAD09615  
40 172.5 7.4 445 2 BAD13230  
41 170.5 7.3 433 2 Q8LFT5  
42 169.5 7.3 433 2 Q9FI78  
43 169.5 7.3 440 2 Q7XXP1  
44 167.5 7.2 441 2 Q7XXP3  
45 166.5 7.1 440 2 Q7XXP2

#### ALIGNMENTS

RESULT 1  
O42692 PRELIMINARY; PRT; 451 AA.  
AC O42692;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Trichothecene 3-O-acetyltransferase.  
GN Names=Tri101;  
OS Gibberella zeae (Fusarium graminearum).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
OX NCBI\_TaxID=5518;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98104153; PubMed=9430709;  
RA Kimura M., Kaneko I., Komiyama M., Takatsuki A., Koshino H., Yoneyama K., Yamaguchi I.;  
RT "Trichothecene 3-O-acetyltransferase protects both the producing organism and transformed yeast from related mycotoxins. Cloning and characterization of."  
RL J. Biol. Chem. 273:1654-1661(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F15;  
RX MEDLINE=98433864; PubMed=9762900;  
RA Kimura M., Matsumoto G., Shingu Y., Yoneyama K., Yamaguchi I.;  
RT "The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the region around Tri101 and characterization of its homologue from Fusarium sporotrichioides."  
RL FEBS Lett. 435:163-168(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98312047; PubMed=9648241;  
RA Kimura M., Shingu Y., Yoneyama K., Yamaguchi I.;  
RT "Features of Tri101, the trichothecene 3-O-acetyltransferase gene, related to the self-defense mechanism in Fusarium graminearum."  
RL Biosci. Biotechnol. Biochem. 62:1033-1036(1998).  
DR EMBL; AB000874; BAA24430.1; -;  
DR EMBL; AB011417; BAA33768.1; -;  
DR EMBL; AB009607; BAA29037.1; -;  
DR FIR; T43733; T43733.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR InterPro; IPR003480; Transferase.  
DR Pfam; PF02458; Transferase; 1.  
KW Transferase.  
SQ SEQUENCE 451 AA; 49496 MW; B2AFBCC59E0B3AAA CRC64;

Query Match 99.1%; Score 2314; DB 2; Length 451;

Best Local Similarity 99.1%; Pred. No. 7.7e-164;

Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAPKIQDITGLQLPGLLSIYTOISLLYPVSDSSQYPTIVSTPFGQIKRSEAVPWAGQV 60

Db 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
 QY 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120  
 Db 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120  
 QY 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180  
 Db 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180  
 QY 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSYKA 240  
 Db 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSYKA 240  
 QY 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300  
 Db 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300  
 QY 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360  
 Db 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360  
 QY 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPETVRRPIFEFVESLMYFMPKPKPD 420  
 Db 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPETVRRPIFEFVESLMYFMPKPKPD 420  
 QY 421 GEFCALSLRDEDMDLKADKEWT 444  
 Db 421 GEFCALSLRDEDMDLKADKEWT 444

RESULT 2

Q9HDE2 ID Q9HDE2 PRELIMINARY; PRT; 444 AA.  
 AC Q9HDE2; 01-MAR-2001 (TremBLrel. 16, Created)  
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Trichothecene 3-O-acetyltransferase (Fragment).  
 OS Gibberella zeae (Fusarium graminearum).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 OX NCBI\_TaxID=5518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL29169, and NRRL28063;  
 RX MEDLINE=20345085; PubMed=10869425;  
 RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;  
 RT "Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab."; Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).  
 RL EMBL; AF212608; AAG43712.1; -;  
 DR EMBL; AF212608; AAG43712.1; -;  
 DR EMBL; AF212605; AAG43712.1; -;  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR InterPro; IPR003480; Transferase.  
 DR Pfam; PF02458; Transferase; 1.  
 KW Transferase.  
 FT NON TER 444 444  
 SQ SEQUENCE 444 AA; 48589 MW; EBCD4ABE2BABF8F5 CRC64;

Query Match 98.4%; Score 2296; DB 2; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-162;  
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
 Db 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
 QY 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120  
 Db 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120

QY 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180  
 Db 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180  
 QY 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSYKA 240  
 Db 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFKFSYKA 240  
 QY 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300  
 Db 241 MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPAWG 300  
 QY 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360  
 Db 301 VSNYPGLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLNHNPKD 360  
 QY 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPETVRRPIFEFVESLMYFMPKPKPD 420  
 Db 361 SNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPETVRRPIFEFVESLMYFMPKPKPD 420  
 QY 421 GEFCALSLRDEDMDLKADKEWT 444  
 Db 421 GEFCALSLRDEDMDLKADKEWT 444

RESULT 3

Q9HDE5 ID Q9HDE5 PRELIMINARY; PRT; 444 AA.  
 AC Q9HDE5; 01-MAR-2001 (TremBLrel. 16, Created)  
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Trichothecene 3-O-acetyltransferase (Fragment).  
 OS Gibberella zeae (Fusarium graminearum).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 OX NCBI\_TaxID=5518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL28336, NRRL5883, NRRL6394, and NRRL13383;  
 RX MEDLINE=20345085; PubMed=10869425;  
 RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;  
 RT "Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab."; Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).  
 RL EMBL; AF212606; AAG43713.1; -;  
 DR EMBL; AF212602; AAG43709.1; -;  
 DR EMBL; AF212603; AAG43710.1; -;  
 DR EMBL; AF212604; AAG43711.1; -;  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR InterPro; IPR003480; Transferase.  
 DR Pfam; PF02458; Transferase; 1.  
 KW Transferase.  
 FT NON TER 444 444  
 SQ SEQUENCE 444 AA; 48615 MW; E2233359B5D4A800 CRC64;

Query Match 98.2%; Score 2291; DB 2; Length 444;  
 Best Local Similarity 99.8%; Pred. No. 3.9e-162;  
 Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
 Db 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
 QY 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120  
 Db 61 KAEIGSEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIIAPRK 120  
 QY 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180  
 Db 121 TLPIGPGTGPDDPKPVILLQGLFIKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

QY	181	TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKA	240
DB	181	TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKA	240
QY	241	MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	300
DB	241	MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	300
QY	301	VSNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPK	360
DB	301	VSNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPK	360
QY	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVESLMYFMPKXPD	420
DB	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVESLMYFMPKXPD	420
QY	421	GEFCAALSRLDEDMDLKADKEWT	444
DB	421	GEFCAALSRLDEDMDLKADKEWT	444
RESULT 4			
ID	Q6J1Y2	PRELIMINARY;	PRT; 442 AA.
AC	Q6J1Y2;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Trichothecene-3-O-acetyltransferase (Fragment)		
OS	Gibberella zeae (Fusarium graminearum)		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.		
OX	NCBI_TaxID=5518;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NRRL34079, and NRRL31084;		
RX	PubMed=15121083;		
RA	O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;		
RT	"Genetical concordance between the mating type locus and seven		
RT	other nuclear genes supports formal recognition of nine		
RT	phylogenetically distinct species within the Fusarium graminearum		
RT	clade."		
RL	Fungal Genet. Biol. 41:600-623 (2004).		
DR	EMBL; AY452808; AAT45943.1; -.		
DR	EMBL; AY452807; AAT45942.1; -.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	InterPro; IPR003480; Transferase.		
DR	Pfam; PF02458; Transferase; 1.		
KW	Transferase.		
FT	NON TER		
FT	NON TER		
FT	NON TER		
SQ	SEQUENCE 442 AA; 48387 MW; 233AD67C82C4C9AF CRC64;		
Query Match			
Best Local Similarity 98.0%; Score 2287; DB 2; Length 442;			
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	3	FKIQLDTLQGLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA	62
DB	1	FKIQLDTLQGLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA	60
QY	63	EGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIIAPKTL	122
DB	61	EGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIIAPKTL	120
QY	123	PIPGTGPDPDPKPVILLQLNFIKGGLILTVNGHGMVGDQDAVIRLLSKACRNDPFE	182
DB	121	PIPGTGPDPDPKPVILLQLNFIKGGLILTVNGHGMVGDQDAVIRLLSKACRNDPFE	180
QY	183	EEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKMS	242
DB	181	EEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKMS	240

QY	243	ELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	302
DB	241	ELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	300
QY	303	NNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPKSN	362
DB	301	NNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPKSN	360
QY	363	VSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVESLMYFMPKXPDGE	422
DB	361	VSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVESLMYFMPKXPDGE	420
QY	423	FCAALSRLDEDMDLKADKEWT	444
DB	421	FCAALSRLDEDMDLKADKEWT	442
RESULT 5			
ID	Q9HF40	PRELIMINARY;	PRT; 444 AA.
AC	Q9HF40;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Trichothecene 3-O-acetyltransferase (Fragment)		
OS	Gibberella zeae (Fusarium graminearum)		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.		
OX	NCBI_TaxID=5518;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NRRL28439;		
RX	MEDLINE=20345085; PubMed=10869425;		
RA	O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;		
RT	"Gene genealogies reveal global phylogeographic structure and		
RT	reproductive isolation among lineages of Fusarium graminearum, the		
RT	fungus causing wheat scab."		
RL	Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).		
DR	EMBL; AF212607; AAG43714.1; -.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	InterPro; IPR003480; Transferase.		
DR	Pfam; PF02458; Transferase; 1.		
KW	Transferase.		
FT	NON TER		
FT	NON TER		
SQ	SEQUENCE 444 AA; 48625 MW; 317A7085872A8796 CRC64;		
Query Match			
Best Local Similarity 97.9%; Score 2286; DB 2; Length 444;			
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	MAFKIQLDTLQGLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV	60
DB	1	MAFKIQLDTLQGLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV	60
QY	61	KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIIAPRK	120
DB	61	KAEGISEGNTGTSFIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIIAPRK	120
QY	121	TIPIPGTGPDPDPKPVILLQLNFIKGGLILTVNGHGMVGDQDAVIRLLSKACRNDPF	180
DB	121	TIPIPGTGPDPDPKPVILLQLNFIKGGLILTVNGHGMVGDQDAVIRLLSKACRNDPF	180
QY	181	TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKA	240
DB	181	TEEMTAMNLDRTIIVPYLNTYIGPEVDHQIVKADVAGDAVLTPVSASNAFFTFSPKA	240
QY	241	MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	300
DB	241	MSELKDAATKTLDASTKFPVSTDDALSFTWKSASRVRLERIDGSAPTEFCRAVDARPAWG	300
QY	301	VSNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPK	360
DB	301	VSNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLNHNPK	360



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361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
|||||
361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
|||||
421 GECCAALSRLDEDMRLKADKEWT 444
|||||
421 GECCAALSRLDEDMRLKADKEWT 444
|||||

RESULT 7
Q9HDE8 PRELIMINARY; PRT; 444 AA.
ID Q9HDE8
AC Q9HDE8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL28720, NRRL6101, NRRL13818, and NRRL26156;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212600; AAG43707.1; -
DR EMBL; AF212597; AAG43704.1; -
DR EMBL; AF212598; AAG43705.1; -
DR EMBL; AF212599; AAG43706.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON_TER
SQ SEQUENCE 444 444
DA814DED9578E7E CRC64;

Query Match 97.5%; Score 2276; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 5.1e-161;
Matches 440; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDPSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPNMFENIIAPRK 120
DB 61 KAEGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPNMFENIIAPRK 120
QY 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
DB 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDKRTIVPYLNTIGPEVDHQIVKADVAGGDVAVLPVSASWAFTEFSPKA 240
DB 181 TEEMTAMNLDKRTIVPYLNTIGPEVDHQIVKADVAGGDVAVLPVSASWAFTEFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSAPFWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSAPFWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMTHNSTIGEANESLGATASRLSELDPASMRQTRGLATYLHNNDPK 360
DB 301 VSNYPGLLQNMTHNSTIGEANESLGATASRLSELDPASMRQTRGLATYLHNNDPK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
QY 421 GECCAALSRLDEDMRLKADKEWT 444
|||||

361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
|||||
361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
|||||
421 GECCAALSRLDEDMRLKADKEWT 444
|||||
421 GECCAALSRLDEDMRLKADKEWT 444
|||||

RESULT 6
Q9HDF3 PRELIMINARY; PRT; 444 AA.
ID Q9HDF3
AC Q9HDF3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL28721, NRRL28436, NRRL28723, NRRL29010, and NRRL26752;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212601; AAG43708.1; -
DR EMBL; AF212582; AAG43689.1; -
DR EMBL; AF212583; AAG43690.1; -
DR EMBL; AF212584; AAG43691.1; -
DR EMBL; AF212594; AAG43701.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON_TER
SQ SEQUENCE 444 444
CB8FAP5772696775 CRC64;

Query Match 97.6%; Score 2277; DB 2; Length 444;
Best Local Similarity 99.1%; Pred. No. 4.3e-161;
Matches 440; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQDLTLGQLPGLLSIYQISLLYPVSDPSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPNMFENIIAPRK 120
DB 61 KAEGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTIEGMRKAGYPNMFENIIAPRK 120
QY 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
DB 121 TLPIGFGTGPDPKPVILLQLNFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDKRTIVPYLNTIGPEVDHQIVKADVAGGDVAVLPVSASWAFTEFSPKA 240
DB 181 TEEMTAMNLDKRTIVPYLNTIGPEVDHQIVKADVAGGDVAVLPVSASWAFTEFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSAPFWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSAPFWKSASRVRLERIDGSAPTFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMTHNSTIGEANESLGATASRLSELDPASMRQTRGLATYLHNNDPK 360
DB 301 VSNYPGLLQNMTHNSTIGEANESLGATASRLSELDPASMRQTRGLATYLHNNDPK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420
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Db 421 GEFCALSLRDEDMDLKADKEWT 444
RESULT 8
Q9HF42
ID Q9HF42 PRELIMINARY; PRT; 444 AA.
AC Q9HF42
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL26755; PubMed=10869425;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR ENBL; AP212595; AAG43702.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48682 MW; 242895FE652F3E16 CRC64;

Query Match 97.5%; Score 2276; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 5.1e-161;
Matches 439; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAPKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQV 60
DB 1 MAPKIQDLTGLQPLGLLSIYQISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120
DB 61 KAEGISEGNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIIAPRK 120
QY 121 TLPFGTGTGDDPKPVILLQLNFIKGLILTVNGHGMDMVGDQDAVIRLLSKACRNDPF 180
DB 121 TLPFGTGTGDDPKPVILLQLNFIKGLILTVNGHGMDMVGDQDAVIRLLSKACRNDPF 180
QY 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDAVLTVPVSASWAFFTSPKA 240
DB 181 TEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDAVLTVPVSASWAFFTSPKA 240
QY 241 MSELKDAATKTLDASTKFTVSTDALLSAFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
DB 241 MSELKDAATKTLDASTKFTVSTDALLSAFTWKSASRVRLERIDGSAPTEFCRAVDARPMG 300
QY 301 VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
DB 301 VSNYPGLLQNMITYHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNPK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEVTRRPIFPVPSLMTFMPKKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPEVTRRPIFPVPSLMTFMPKKPD 420
QY 421 GEFCALSLRDEDMDLKADKEWT 444
DB 421 GEFCALSLRDEDMDLKADKEWT 444

RESULT 10
Q9HDN2
ID Q9HDN2 PRELIMINARY; PRT; 444 AA.
AC Q9HDN2
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

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OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28718, NRRL2903, and NRRL28585;
RA MEDLINE=20345085; PubMed=10869425;
RX O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212587; AAG43694.1; -.
DR EMBL; AF212585; AAG43692.1; -.
DR EMBL; AF212586; AAG43693.1; -.
DR GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444
SQ SEQUENCE 444 AA; 48638 MW; 12A8337C5320COAD CRC64;

Query Match 97.3%; Score 2272; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 1e-160;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAFKIQDITLGLPGLLSIYTIQISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQDITLGLPGLLSIYTIQISLLYPVSDPSQYPAIVSTFEOGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
DB 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
QY 121 TLPIGGCTGDDPKPVILLQLNFIKGLLITVNGHGMVMVQDQDAVIRLLSKACRNDPF 180
DB 121 TLPIGGCTGDDPKPVILLQLNFIKGLLITVNGHGMVMVQDQDAVIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
DB 181 TEEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
QY 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPAMG 300
DB 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPAMG 300
QY 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
DB 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKPKPD 420
QY 421 GFCAALSRLDEDMRLKADKEWT 444
DB 421 GFCAALSRLDEDMRLKADKEWT 444

RESULT 11
Q9HD15 PRELIMINARY; PRT; 444 AA.
AC Q9HD15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL29148, and NRRL25797;
RX MEDLINE=20345085; PubMed=10869425;

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RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212589; AAG43696.1; -.
DR EMBL; AF212588; AAG43695.1; -.
DR GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444
SQ SEQUENCE 444 AA; 48680 MW; 69A6A48E702227C3 CRC64;

Query Match 97.3%; Score 2271; DB 2; Length 444;
Best Local Similarity 98.9%; Pred. No. 1.2e-160;
Matches 439; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAFKIQDITLGLPGLLSIYTIQISLLYPVSDSSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
DB 1 MAFKIQDITLGLPGLLSIYTIQISLLYPVSDPSQYPTIVSTFEOGLKRFSEAVPWVAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
DB 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFMFENIIAPRK 120
QY 121 TLPIGGCTGDDPKPVILLQLNFIKGLLITVNGHGMVMVQDQDAVIRLLSKACRNDPF 180
DB 121 TLPIGGCTGDDPKPVILLQLNFIKGLLITVNGHGMVMVQDQDAVIRLLSKACRNDPF 180
QY 181 TEEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKADVAGGDAVLTVPVSASWAFFTSPKA 240
DB 181 TEEEMTAMNLDRTIIVPYLENTYIGPEVDHQIVKPDVAGGDAVLTVPVSASWAFFTSPKA 240
QY 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPAMG 300
DB 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPAMG 300
QY 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
DB 301 VSNYPGLLQNNYTHNSTIGEIANESLGATASRLSELDPASMRQTRGLATYLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKPKPD 420
QY 421 GFCAALSRLDEDMRLKADKEWT 444
DB 421 GFCAALSRLDEDMRLKADKEWT 444

RESULT 12
Q9HDE0 PRELIMINARY; PRT; 444 AA.
AC Q9HDE0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25805, and NRRL25491;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212613; AAG43720.1; -.

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DR EMBL; AF212612; AAG43719.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48650 MW; EDE94D869BB0B188 CRC64;

Query Match
Best Local Similarity 97.0%; Score 2265; DB 2; Length 444;
Matches 437; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAPKIQDLTGLQGLLSIYTIQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
DB 1 MAPKIQDLTGLQGLLSIYTIQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWVAGQV 60
QY 61 KAEGISSEGTGTSFIYVFPEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFDENIIAPRK 120
DB 61 KAEGISSEGTGTSFIYVFPEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFDENIIAPRK 120
QY 121 TLPFGTGPDDPKPVILLQLNFIKGGILITVNGHQHGMVQGDVAVIRLLSKACRNDPFF 180
DB 121 TLPFGTGPDDPKPVILLQLNFIKGGILITVNGHQHGMVQGDVAVIRLLSKACRNDPFF 180
QY 181 TBEETAMNLDRTIYVPLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
DB 181 TBEETAMNLDRTIYVPLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKA 240
QY 241 MSELKDAAKTLDASTKFKVSTDDALSATFKWSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAAKTLDASTKFKVSTDDALSATFKWSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNMITYHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYVHNPNPK 360
DB 301 VSNYPGLLQNMITYHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYVHNPNPK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVPSLAMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVPSLAMYFMPKPKPD 420
QY 421 GEFCAALSURDEDMRLKADKEWT 444
DB 421 GEFCAALSURDEDMRLKADKEWT 444

RESULT 13
Q6JIX6 PRELIMINARY; PRT; 441 AA.
AC Q6JIX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Trichothecene-3-O-acetyltransferase (Fragment).
OS Fusarium brasiliicum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=281087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL31281; and NRRL31238;
RX PubMed=15121083;
RA O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;
RT "Genealogical concordance between the mating type locus and seven
RT other nuclear genes supports formal recognition of nine
RT phylogenetically distinct species within the Fusarium graminearum
RT clade.";
RL Fungal Genet. Biol. 41:600-623 (2004).
DR EMBL; AY452814; AAT45949.1; -.
DR EMBL; AY452813; AAT45948.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.

FT NON TER 444 444
SQ SEQUENCE 444 AA; 48641 MW; 63DC08FAFF9889E5 CRC64;

Query Match
Best Local Similarity 96.7%; Score 2257; DB 2; Length 444;
Matches 435; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

FT NON TER 1 1
SQ SEQUENCE 441 AA; 48319 MW; 9E36C23E86E4EB61 CRC64;

Query Match
Best Local Similarity 96.9%; Score 2262; DB 2; Length 441;
Matches 437; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 KIQDLTGLQGLLSIYTIQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA 63
DB 1 KIQDLTGLQGLLSIYTIQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWVAGQVKA 60
QY 64 GISEGNTGTSFIYVFPEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFDENIIAPKTL 123
DB 61 GISEGNTGTSFIYVFPEDVPRVVKDLRDDPSAPTEIEGRKAGYPMAMFDENIIAPKTL 120
QY 124 IGPGTGPDDPKPVILLQLNFIKGGILITVNGHQHGMVQGDVAVIRLLSKACRNDPTEE 183
DB 121 IGPGTGPDDPKPVILLQLNFIKGGILITVNGHQHGMVQGDVAVIRLLSKACRNDPTEE 180
QY 184 EMTAMNLDRTIYVPLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKAMSE 243
DB 181 EMTAMNLDRTIYVPLENTYIGPEVDHQIVKADVAGDAVLTPVSASWAFPTSPKAMSE 240
QY 244 LKDAATKTLDASTKFKVSTDDALSATFKWSASRVRLERIDGSAPTEFCRAVDARPAWG 303
DB 241 LKDAATKTLDASTKFKVSTDDALSATFKWSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 304 NYPGLLQNMITYHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYVHNPNKSNV 363
DB 301 NYPGLLQNMITYHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYVHNPNKSNV 360
QY 364 SLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVPSLAMYFMPKPKDGEF 423
DB 361 SLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFPVPSLAMYFMPKPKDGEF 420
QY 424 CAALSURDEDMRLKADKEWT 444
DB 421 CAALSURDEDMRLKADKEWT 441

RESULT 14
Q9HF38 PRELIMINARY; PRT; 444 AA.
AC Q9HF38;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (Fragment).
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL13393;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212614; AAG43721.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48641 MW; 63DC08FAFF9889E5 CRC64;
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QY 1 MAFKIQLDTLQGLLSIYTOISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQV 60
DB 1 MAFKIQLDTLQGLLSIYTOISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
DB 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
QY 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
DB 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
QY 181 TEEETAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 240
DB 181 TEEETAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNNYHNSITGEIANESLGATASRLRSELDPASMRQTRGLATYLLHNNPDK 360
DB 301 VSNYPGLLQNNYHNSITGEIANESLGATASRLRSELDPASMRQTRGLATYLLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
QY 421 GEFCAALSRLRDEDMDLKADKEWT 444
DB 421 GEFCAALSRLRDEDMDLKADKEWT 444
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## RESULT 15

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Q9HF39 PRELIMINARY; PRT; 444 AA.
AC Q9HF39
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trichothecene 3-O-acetyltransferase (fragment).
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=NRRL13721;
RX MEDLINE=20345085; PubMed=10869425;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab."
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
DR EMBL; AF212611; AAC43718.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
FT NON TER 444 444
SQ SEQUENCE 444 AA; 48694 MW; FCA1047B43207194 CRC64;
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Query Match 96.6%; Score 2255; DB 2; Length 444;  
Best Local Similarity 98.0%; Pred. No. 1.9e-159;  
Matches 435; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 1 MAFKIQLDTLQGLLSIYTOISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQV 60
DB 1 MAFKIQLDTLQGLLSIYTOISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQV 60
QY 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
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DB 61 KAEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
QY 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
DB 121 TLPFGTGPDPKPVILLQNLFIKGLLITVNGHGMVGDVAVIRLLSKACRNDPF 180
QY 181 TEEETAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 240
DB 181 TEEETAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFKVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
QY 301 VSNYPGLLQNNYHNSITGEIANESLGATASRLRSELDPASMRQTRGLATYLLHNNPDK 360
DB 301 VSNYPGLLQNNYHNSITGEIANESLGATASRLRSELDPASMRQTRGLATYLLHNNPDK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKPKPD 420
QY 421 GEFCAALSRLRDEDMDLKADKEWT 444
DB 421 GEFCAALSRLRDEDMDLKADKEWT 444
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Search completed: January 23, 2005, 19:49:07  
JOB time : 113 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 23, 2005, 19:32:07 ; Search time 32 Seconds  
(without alignments)  
934.669 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAPKIQDLTGLPGLLSIY.....EDMDRLKADKWKYQYVG 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	3	US-09-538-414-6
2	2334	100.0	451	4	US-10-074-279-6
3	1860.5	79.7	459	3	US-09-538-414-2
4	1860.5	79.7	459	4	US-10-074-279-2
5	962.5	41.2	474	3	US-09-538-414-8
6	962.5	41.2	474	4	US-10-074-279-8
7	142	6.1	448	3	US-09-457-046B-56
8	141.5	6.1	436	3	US-09-457-046B-62
9	134	5.7	448	1	US-08-207-904-2
10	134	5.7	448	1	US-08-207-904-17
11	132	5.6	439	3	US-09-457-046B-28
12	130.5	5.6	451	3	US-09-457-046B-69
13	126.5	5.4	435	3	US-09-457-046B-60
14	125.5	5.4	439	3	US-09-457-046B-68
15	124	5.3	445	3	US-09-457-046B-73
16	122	5.2	433	3	US-09-457-046B-66
17	121.5	5.2	306	3	US-09-457-046B-22
18	121.5	5.2	482	3	US-09-457-046B-63
19	118	5.1	450	3	US-09-457-046B-67
20	117	5.0	830	4	US-09-562-737-34
21	113	4.8	440	3	US-09-457-046B-45
22	112	4.8	441	3	US-09-457-046B-54
23	110.5	4.7	1858	4	US-09-489-039A-11380
24	106.5	4.6	303	3	US-09-457-046B-20
25	105.5	4.5	446	3	US-09-457-046B-74
26	105.5	4.5	3724	2	US-08-804-227C-10
27	105.5	4.5	3724	2	US-08-804-198-4

28	104.5	4.5	769	4	US-09-248-796A-18265	Sequence 18265, A
29	104.5	4.5	1337	3	US-08-854-585-2	Sequence 2, Appli
30	104.5	4.5	1337	4	US-09-447-533-2	Sequence 2, Appli
31	104.5	4.5	1337	5	PCT-US95-05512-2	Sequence 2, Appli
32	104	4.5	302	3	US-09-457-046B-24	Sequence 24, Appli
33	103.5	4.4	458	3	US-09-457-046B-61	Sequence 61, Appli
34	102.5	4.4	810	4	US-09-583-110-4352	Sequence 4352, Ap
35	102	4.4	802	3	US-09-147-236-4	Sequence 4, Appli
36	102	4.4	802	4	US-09-522-474-4	Sequence 4, Appli
37	100	4.3	461	3	US-09-457-046B-70	Sequence 70, Appli
38	99.5	4.3	455	3	US-09-457-046B-72	Sequence 72, Appli
39	99.5	4.3	1289	2	US-08-542-003-2	Sequence 2, Appli
40	99.5	4.3	1289	2	US-08-322-760A-2	Sequence 2, Appli
41	99.5	4.3	1289	4	US-09-236-949-2	Sequence 2, Appli
42	99	4.2	306	3	US-09-457-046B-2	Sequence 2, Appli
43	98.5	4.2	560	2	US-08-981-690-2	Sequence 2, Appli
44	98.5	4.2	610	4	US-09-455-777-2	Sequence 2, Appli
45	97	4.2	347	4	US-09-328-352-7107	Sequence 7107, Ap

ALIGNMENTS

RESULT 1  
US-09-538-414-6  
; Sequence 6, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Fusarium graminearum  
US-09-538-414-6

Query Match	100.0%	Score	2334	DB	3	Length	451
Best Local Similarity	100.0%	Pred. No.	1.1e-233				
Matches	451	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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Db	1	MAPKIQDLTGLPGLLSIY	TOISLLYPVSDSQYPTIVSTFQGLKRFSEAVPWAGQV	60			
Qy	61	KAEGISGNTGTSFIVPFEDVPRVVVKLDLDDPSAPTIEGRKAGYPMAMFENIAPRK	120				
Db	61	KAEGISGNTGTSFIVPFEDVPRVVVKLDLDDPSAPTIEGRKAGYPMAMFENIAPRK	120				
Qy	121	TLPIGPGTGPDDPKPVILLQLNFIKGLLITVNGQHGAMDVGQDAVIRLLSKACRNDPF	180				
Db	121	TLPIGPGTGPDDPKPVILLQLNFIKGLLITVNGQHGAMDVGQDAVIRLLSKACRNDPF	180				
Qy	181	TEBEMTAMNLDRTIIVPLENYTIGPEVDHQIKVADVAGDVAVLTPVSASWAFFTSPKA	240				
Db	181	TEBEMTAMNLDRTIIVPLENYTIGPEVDHQIKVADVAGDVAVLTPVSASWAFFTSPKA	240				
Qy	241	MSELKDAATKTLDASTKFTVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPMG	300				
Db	241	MSELKDAATKTLDASTKFTVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDARPMG	300				
Qy	301	VSNVYGLLONWYTHNSTTGEIANESIGATASRLRSELDPASWRQTRGLATVILHNNPDK	360				
Db	301	VSNVYGLLONWYTHNSTTGEIANESIGATASRLRSELDPASWRQTRGLATVILHNNPDK	360				

Db 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYLNHNPDK 360  
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Qy 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451  
Db 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451

## RESULT 2

US-10-074-279-6  
; Sequence 6, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Fusarium graminearum  
US-10-074-279-6

Query Match 100.0%; Score 2334; DB 4; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.1e-233;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAFKIQDLTGQLPGLLSIYTOISLVPVSDSSQYPTIVSTFPGQKRFSEAVPWVAGQV 60  
Db 1 MAFKIQDLTGQLPGLLSIYTOISLVPVSDSSQYPTIVSTFPGQKRFSEAVPWVAGQV 60  
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Db 61 KASGISGNTGTSTFVPPFEDVPRVVKDLRDDPSAPTIEGRKAGYPMAMFENIIAPRK 120  
Qy 121 TLPIGPGTGDDPKPVILLQNLFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 180  
Db 121 TLPIGPGTGDDPKPVILLQNLFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 180  
Qy 181 TEEMTAMNLDRTIIVPLENYTIGPEVDHQIVKADVAGDVLTPVSASWAFPTSPKA 240  
Db 181 TEEMTAMNLDRTIIVPLENYTIGPEVDHQIVKADVAGDVLTPVSASWAFPTSPKA 240  
Qy 241 MSELKDAATKTLDASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG 300  
Db 241 MSELKDAATKTLDASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG 300  
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Db 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYLNHNPDK 360  
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Qy 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451  
Db 421 GEFCALSLRDEDMRLKADKWKTKYQYVG 451

## RESULT 3

US-09-538-414-2  
; Sequence 2, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Fusarium sporotrichioides  
US-09-538-414-2

Query Match 79.7%; Score 1860.5; DB 3; Length 459;  
Best Local Similarity 77.6%; Pred. No. 2e-184;  
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;  
Qy 2 AFKIQDLTGQLPGLLSIYTOISLVPVSDSSQYPTIVSTFPGQKRFSEAVPWVAGQV 61  
Db 11 SFDIELDIIOQOPPLLSIYTOISLVPVSDSSQYPTIVSTFPGQKRFSEAVPWVAGQV 70  
Qy 62 AEGISGNTGTSTFVPPFEDVPRVVKDLRDDPSAPTIEGRKAGYPMAMFENIIAPRK 121  
Db 71 TEGISGNTGTSTFVPPFEDVPRVVKDLRDDPSAPTIEGRKAGYPMAMFENIIAPRK 130  
Qy 122 LPPIGPGTGDDPKPVILLQNLFIKGGILITVNGQHGMDMVGDQDAVIRLLSKACRNDPF 181  
Db 131 LAIGPFGNGPDKPVILLQNLFIKGGILITVNGQHGMDMTGQDAIIRLLSKACRNEST 190  
Qy 182 TEEMTAMNLDRTIIVPLENYTIGPEVDHQIVKADVAGDVLTPVSASWAFPTSPKA 241  
Db 191 EBEISAMNLDRTIIVPLENYTIGPEVDHQIVKADVAGDVLTPVSASWAFPTSPKA 249  
Qy 242 SELKDAATKTLDASTKVFSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG 301  
Db 250 SELKDAATKTLDASTKVFSTDDALSAFIWQSTSRVRLARLDASTPTFCRAVDMRGMGV 309  
Qy 302 SNYPGLLQNMVTHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYLNHNPDKS 361  
Db 310 SSTYPCLLQNMVTHDSTVAEIANEPLGATASRLSELSDRLRRRTQALATYMHGLPDKS 369  
Qy 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 421  
Db 370 VSVSLTADANPSSIMLSSWAKVGCWEYDFGLGKGPESVRRPFRFPFESLMYFMPKKPD 429  
Qy 422 EFCALSLRDEDMRLKADKWKTKYQYVG 451  
Db 430 EFTASISLRDEDMERLKADEEWTKYAKYIG 459

## RESULT 4

US-10-074-279-2  
; Sequence 2, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Fusarium sporotrichioides  
US-10-074-279-2

Query Match 79.7%; Score 1860.5; DB 4; Length 459;  
Best Local Similarity 77.6%; Pred. No. 2e-184;  
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

Qy 2 AFKIQDITGQLPGLLSIYTOISLLYPVSDSQYPTIVSTFEOGLKRFSEAVPWVAGQVK 61  
Db 11 SPDIELDIQQPPLLSIYTOISLLYPVSDSQYPTIVSTFEOGLKRLSQTFFWVAGQVK 70  
Qy 62 AEGISEGNTGTSFIYPPFEDVPRVVKDLRDDSPAPTIEGMRKAGYPMAMFENIAPRKT 121  
Db 71 TEGISEGNTGTSKIIPYEETPRLVKDLRDDSSAPTIEGLRAGPPEMFEDENVAPRKT 130  
Qy 122 LPIGPOTGDDPKPVILLQNLTKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPPT 181  
Db 131 LAIFGNGFNDPKPVILLQNLTKGLILTVNGQHGAMDMTQDAIIRLLSKACRNEST 190  
Qy 182 EEMTAMNLDKRTIVPYLENTYIGPEVDHQIVKADVAGGDAVLTVPVSAWAPFTFSPKAM 241  
Db 191 EEEISAMNLDKRTVPLENYKVGPELDHQIAKPAPA-GDAPPAPAKASWAFSTPKAL 249  
Qy 242 SELKDAATKTLDASTKFVSTDDALSFAFIWKSASRVLERIDGSAPTEFCRAVDARPAQV 301  
Db 250 SELKDAATKTLDASSKFVSTDDALSFAFIWQTSRVLEALDLASTPTEFCRAVDMRGPVG 309  
Qy 302 SNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLNHPDKS 361  
Db 310 SSTYPGLLQNMVTHDSTVAIANEPICATASRLRSELNSDRIRRTQALATYHGLPDKS 369  
Qy 362 NVSLTADADPSTVMLSSWAKVGLMDYDFGLGKGPETVRRPIFEPVESLAMYFMPKPKPDG 421  
Db 370 SVSLTADANPSSIMLSSWAKVGCWEYDFGLGKGPESVRRPRFEPFESLAMYFMPKPKPDG 429  
Qy 422 EFCALSLRDEDMRLKADKEWTKYAOYVG 451  
Db 430 EFTASISLRDEMERLKADEEWTYAKYIG 459

RESULT 5  
US-09-538-414-8  
; Sequence 8, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 474  
; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae  
US-09-538-414-8

Query Match 41.2%; Score 962.5; DB 3; Length 474;  
Best Local Similarity 44.4%; Pred. No. 4.9e-91;  
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

Qy 6 QLDITGQLPGLLSIYTOISLLYPVSDSQYPTIVSTFEOGLKRFSEAVPWVAGQVKAEGI 65  
Db 22 QLDILGQQPSLYKLYTCISYRVPDPSAHDHIVNTLTRGLTAKNFQWLAGNVVNEGA 81  
Qy 66 SEGNTGTSFIYPPFEDVPRVVKDLRDDSPAPTIEGMRKAGYPMAMFENIAPRKT-LPI 124  
Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFFIYMLDEKTFAPCMTINPP 140  
Qy 125 GPGTG-PDDPKPVILLQNLTKGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTBE 183  
Db 141 GNTIGMAAKSGPFAVQANFISGLVLITVNGHNDITQGESIINLANKSCHQKFEFSDE 200  
Qy 184 EMTAMNLDKRTIVPYLENTYIGPEVD--HQIVKA--DVAGGDAVLTVPVSAWAPFTFSP 238  
Db 201 ELLIGNIDKSKSIPLFDE--TWEPTDTTLVHEIVETSRNTSGEEKEQSCSSNTWYVEFSA 259  
Qy 239 KAMSELKDAATKTLDASTKFVSTDDALSFAFIWKSASRVLERIDGSAPTEFCRAVDARPA 298  
Db 260 ISLQNLIRILAMQTCSTGTFKPVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVRK 319  
Qy 299 MGVSNNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDP--SMRQRTGLATYLNH 356  
Db 320 LGLPETYGGLLVNMTFNTGSLKSLDHSGLVGLASQIRRLKDPKVPFLAYNTCALATLSR 379  
Qy 357 NPKDSNVSLTADADPSTVMLSSWAKVGLMDYDFGLGKGPETVRRPIFEPVESLAMYFMP 416  
Db 380 CPDKTKVSIQPIDTLGSLMVSSWAKVSLYDVFDFNLGLGKPKSVRRPRFISLESLEYFMP 439  
Qy 417 KXPDEGFCALSLRDEDMRLKADKEWTKYAOYVG 451  
Db 440 RSSRGMVVALCLRDQWECNLNADKEWTNYATHIG 474

RESULT 6  
US-10-074-279-8  
; Sequence 8, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-074-279-8

Query Match 41.2%; Score 962.5; DB 4; Length 474;  
Best Local Similarity 44.4%; Pred. No. 4.9e-91;  
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

Qy 6 QLDITGQLPGLLSIYTOISLLYPVSDSQYPTIVSTFEOGLKRFSEAVPWVAGQVKAEGI 65  
Db 22 QLDILGQQPSLYKLYTCISYRVPDPSAHDHIVNTLTRGLTAKNFQWLAGNVVNEGA 81



QY 66 SEGNTGTSFIVFEDVPRVVKDLRDDPSAPTIEGRKAGVPMAMFENIAPRKL-PI 124  
DB 82 DEGNTGTVRIVPSDKIP-LIVQDLREDUSAPTMSLEKADFFIYMLDEKTFAPCMTINPP 140  
QY 125 GPGTG-PDDPKVILLQNLFIKGGILITVNGQHGAMDMVGDVIRLLSKACRNDPFTTE 183  
DB 141 GNTIGMAKSGPVFAVQANFISGLGLVITVQHNIMDITQBSIIINLLNKSCHQKPFSE 200  
QY 184 ENTAMNLDKRTIVPVLENTIGPEVD--HQIVKA--DVAGGDVAUTPVIS-ASWAFPTSP 238  
DB 201 ELLIGNIDKSKIPLFDE-TWEPDITLVEHIVETSRTSGEEKQSCSSNSTWAYVFSA 259  
QY 239 KAMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVLEIRIDGSAPTFCRAVDARPA 298  
DB 260 ISLQNLRIILAMOTCTGSKFTVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVVR 319  
QY 299 MGVSNNYPGLLQNMVTHNSTIGEIANESIGATASRLSELDP--SMRQRTGLATYLN 356  
DB 320 LGLPETYPGLVNMVTFNTGSLKSLDKHSLGVLASQIRRLKDPKVPDLAYNTCALATLLSR 379  
QY 357 NPKDSNVSLTADAPDSTVMSLWSAKVGLWDYDFGLGKPKETVRRPIPEPESLWYMP 416  
DB 380 CPDKTKVSIPOPTDITLSGINVSWAKVSLYDVFENLGLGKPKSVRRPRFISLESIIYMP 439  
QY 417 KKPDPGEFCAALSIRDEDMRLKADKWTKYAOVVG 451  
DB 440 RSRGGEVVALCLURDKWELNADKWTNYATHIG 474

## RESULT 7

US-09-457-046B-56  
; Sequence 56, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679  
; CURRENT APPLICATION NUMBER: US/09/457,046B  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Taxus cuspidata  
US-09-457-046B-56

Query Match 6.1%; Score 142; DB 3; Length 448;  
Best Local Similarity 20.5%; Pred. No. 9.2e-06;  
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;  
QY 5 IQDITGQLPGLLSIYQISLLYFVSDSSQYPIVSTFTEQGLKRFSEAVPWVAGQVKAEG 64  
DB 35 LQLSAVDRLEPKMFATFSVAVLVNASSHSIFANPAQIIRQALSKEVQYYPAPFAGRIRQKE 94  
QY 65 ISB-----GNTGTSFIVFEDVPRVVKDLRDDPSAPTIEGRKAGVPMAMFENIAPR 119  
DB 95 NEELEVECTEGALFVEMVNDLSVLRLD-----DAQNASVEQLLF----- 136  
QY 120 KTLPIGPGTGDDPKPVILLQNLFIKGGILITVNGQHGAMDMVGDVIRLLSKACRND- 178  
DB 137 -SLP--ENIQVDLHPLILQVTRFTCGFVGVGVGFHIGICDARGGTQFLQGLADMARGET 193  
QY 179 -PFTTEEWAMNLDKRTIVP-----YLENTYIGPEVDHQIVKADVAGGDVITPVSAWAF 233  
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKFG--LIRQPLKLD-----EICOAS 235  
QY 234 FTFGPKAMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVLEIRIDGSAPTFCRAV 293  
DB 236 FTINSEIINYIKQC---VIEECNEIFSAFVWVWALTW--IARTKAFQIPHENVMMLFGM 290  
QY 294 DARPAMGVSNYPGLLQNMVTHNSTIG-----EIANESIGATASRLSELDPASMR 344

DB 291 DARYFN-----PPLPRG--YYGNAICTSCVNIENQDLLNGSLSRAMWITKSKIPLIEN 343  
QY 345 QRTGLATYLNHNPKDNVSLTADAPDSTVMSLWSAKVGLWDYDFGLG 393  
DB 344 LRSRIVA-----NQSGVD--EIKHENVVFGDWRRLGHEFVDFGSG 383

## RESULT 8

US-09-457-046B-62  
; Sequence 62, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Pacilitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679  
; CURRENT APPLICATION NUMBER: US/09/457,046B  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 62  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-457-046B-62

Query Match 6.1%; Score 141.5; DB 3; Length 436;  
Best Local Similarity 22.2%; Pred. No. 9.9e-06;  
Matches 74; Conservative 56; Mismatches 133; Indels 71; Gaps 14;

QY 135 PVILLQNLFIK-GGLITVNGQHGAMDMVGDVIRLLSKACRN-----DPFTE----- 182  
DB 135 PVLLIQANFFSCGGLVITICVSHKITDATSAMIRGWAESSRGLGITLIFSFTASEVFP 194  
QY 183 ---EEMTAMNLDKRTIVPVLENTYIGPEVDHQIVKADVAGGDVITPVSAWAFPTSPK 239  
DB 195 KPLDELPSKPMDRK-----EEVEE-----MSCVTKRFVFDAS 226  
QY 240 AMSELKDAATKTLDASTKFTVSTDDALSFAIWKASRVLEIRIDGSAPTFCRAVDARPA 299  
DB 227 KIKLRAKARNL---VKNPTRVEAVTALFWRCTKV--SRLSLTP-----RTSVLQILV 277  
QY 300 GVSNNYPGLLQNMVTHNSTIGEIANESIGATASRLSELDPASMRQRTGLATYLNHNP 359  
DB 278 NLRGKVDLSCENTIGNMLSLMLKNEE--AARIQDVVDEI---RRAKEIFSLNCKEMS 332  
QY 360 KSNVSLTADAPDSTV-----MLSSWAKVGLWDYDFGLGKPKETVRRPIPEPVE 409  
DB 333 KSSSRIFELLEIGKVYGRGNEMDLWMSNSWCKLGYDADF--GWGKPVWVTGRGTSHFK 390  
QY 410 SLMYFMPKPKDGEFCAA--LSLDEDMRLKADKE 442  
DB 391 NLMLLIDTK-DGEGIEAWITLITEQMSLFECDOE 423

## RESULT 9

US-08-207-904-2  
; Sequence 2, Application US/08207904  
; Patent No. 5477002  
; GENERAL INFORMATION:  
; APPLICANT: Tuttle, AnnMarie  
; APPLICANT: Crossland, Lyle D.  
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic  
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/207,904  
;/ FILING DATE:  
;/ CLASSIFICATION: 800  
;/ PRIOR APPLICATION NUMBER: US/07/908,242  
;/ FILING DATE:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Lazar, Steven R.  
;/ REGISTRATION NUMBER: 32,618  
;/ REFERENCE/DOCKET NUMBER: CGC 1624  
;/ TELEPHONE: (919)541-8615  
;/ TELEFAX: (919)541-8615  
;/ INFORMATION FOR SEQ ID NO: 2:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 448 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-08-207-904-2

Query Match 5.7%; Score 134; DB 1; Length 448;  
Best Local Similarity 21.7%; Pred. No. 6.2e-05;  
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

QY 21 TQISLLY-----PVSDSQYPTIVSTFEGLKR-----FSEAVPWAGQVKAEG 64  
DB 34 THVPTIYYRFFCHDCLPSTDN-----IIKLTRSLSKALVHFYPLSGRLRWIAG-----S 83  
QY 65 ISENGTGTGFIVPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPR--KTL 122  
DB 84 RLELDCNAGSIVLMEATEAKLDLDLGFSPSP-----DLSLFPFVDYTI 128  
QY 123 PIGPGTGPDDPKPVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179  
DB 129 PI-----DELPLLVQLTKFCGGIALSFAISHAVVD--GQSALYFLTEWASLARGE 179  
QY 180 FTEEMTAMNLDKRTI-----VPYLENTYTIGPEVDHQIVKADVAGDAVLTPVSASW 231  
DB 180 LGNEPFP-----DRKFLRAGEPPIAYPTFEHLQFNP-----PPLLGGSS-- 220  
QY 232 APFTFSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIWKSASRVRL 278  
DB 276 HKFE--QPTNLCICVNIQMPPPKSYFGNAIVDVIANGVSGDITSRPLEYVARRV-- 332  
QY 333 ----AAIKMVTSDYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPNLGI--SW 383  
QY 381 AKVGLWDYDFGLGKPEVRRPIPEFVESLMYFMP-KKPDGEFCALSIRDEMDRLK 438  
DB 384 ISLPLGLDFGWG---KEIHMSPTTHEYDGDVCVILPFGKGDGSLTVAIILOAVHVDAFK 439

RESULT 10

US-08-207-904-17  
; Sequence 17, Application US/08207904  
; Patent No. 5477002  
; GENERAL INFORMATION:  
; APPLICANT: Tuttle, AnnMarie  
; APPLICANT: Crossland, Lyle D.  
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic  
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences  
; NUMBER OF SEQUENCES: 21

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: CIBA-GEIGY Corporation  
;/ STREET: 7 Skyline Drive  
;/ CITY: Hawthorne  
;/ STATE: New York  
;/ COUNTRY: USA  
;/ ZIP: 10532  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/207,904  
;/ FILING DATE:  
;/ CLASSIFICATION: 800  
;/ PRIOR APPLICATION NUMBER: US/07/908,242  
;/ FILING DATE:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Lazar, Steven R.  
;/ REGISTRATION NUMBER: 32,618  
;/ REFERENCE/DOCKET NUMBER: CGC 1624  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (919)541-8615  
;/ TELEFAX: (919)541-8689  
;/ INFORMATION FOR SEQ ID NO: 17:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 448 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-08-207-904-17

Query Match 5.7%; Score 134; DB 1; Length 448;  
Best Local Similarity 21.7%; Pred. No. 6.2e-05;  
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

QY 21 TQISLLY-----PVSDSQYPTIVSTFEGLKR-----FSEAVPWAGQVKAEG 64  
DB 34 THVPTIYYRFFCHDCLPSTDN-----IIKLTRSLSKALVHFYPLSGRLRWIAG-----S 83  
QY 65 ISENGTGTGFIVPFEDPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPR--KTL 122  
DB 84 RLELDCNAGSIVLMEATEAKLDLDLGFSPSP-----DLSLFPFVDYTI 128  
QY 123 PIGPGTGPDDPKPVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179  
DB 129 PI-----DELPLLVQLTKFCGGIALSFAISHAVVD--GQSALYFLTEWASLARGE 179  
QY 180 FTEEMTAMNLDKRTI-----VPYLENTYTIGPEVDHQIVKADVAGDAVLTPVSASW 231  
DB 180 LGNEPFP-----DRKFLRAGEPPIAYPTFEHLQFNP-----PPLLGGSS-- 220  
QY 232 APFTFSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIWKSASRVRL 278  
DB 221 ----BEEKNETKGSMLKTKHQVEMLRKANQGNQGRSYTRYEVVTAHWRACKARG 275  
QY 279 ERIDGSAPTFCRAVDARPA--GVSNNTYPGLLQNNMTYHNTSTIGEIANESLGATASRLRS 336  
DB 276 HKFE--QPTNLCICVNIQMPPPKSYFGNAIVDVIANGVSGDITSRPLEYVARRV-- 332  
QY 337 ELDPAQMORTGLAT-----YLHNNPDKNSVLTAD-----ADPSTSVMLSSW 380  
DB 333 ----AAIKMVTSDYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPNLGI--SW 383  
QY 381 AKVGLWDYDFGLGKPEVRRPIPEFVESLMYFMP-KKPDGEFCALSIRDEMDRLK 438  
DB 384 ISLPLGLDFGWG---KEIHMSPTTHEYDGDVCVILPFGKGDGSLTVAIILOAVHVDAFK 439

RESULT 11  
US-09-457-046B-28

Sequence 28, Application US/09457046B  
Patent No. 6287835  
GENERAL INFORMATION:  
APPLICANT: Croteau, Rodney et al.  
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
FILE REFERENCE: 53679  
CURRENT APPLICATION NUMBER: US/09/457,046B  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 439  
TYPE: PRT  
ORGANISM: Taxus cuspidata  
US-09-457-046B-28

Query Match 5.7%; Score 132; DB 3; Length 439;  
Best Local Similarity 20.0%; Pred. No. 9.7e-05;  
Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21;

Qy 5 IQLDTLGQLPGLLSIYQISLLYPVSDSSQYPTIVST-----PEOGLKRFSEAVPWVAGQ 59  
Db 27 LQLSSDNLPLFVGRGSIYNALLIYNASPS---PTMISADPAKPIREMAKILIVYPPFAGR 83  
Qy 60 VK-----AEGISEGNTGTSFIVPFEDVPRVYVVKLDLDDPSAPTIEGMRKAGYPMAMP 111  
Db 84 LRETENGDLVECTGE---GAMFLEAMADNLSVLGDF---DSDNPSFQOL-----LF 130  
Qy 112 DENIIPRKTLPFGPTGDDPKPVILLQNLFIKGLLITVNGOHGAMVQDQAVIRLL 171  
Db 131 -----SLPL--DTNFKDLVLLVQVTRFTCGGVFVGVSPHHGVCDGRGAQFLKGL 179  
Qy 172 SKACRN-----DPFTEETAMNLDRTIVPYLENYTTGPEVDHQIVKRVAGGDAVL 225  
Db 180 AEWARGEVKLSLEPIWNRRLKID-DPKYLOPHFELRAPSIVEKIVQ-----227  
Qy 226 PVSASWAFFTFSPKAMSELKDAATKTLDASTKTVSDTDLASFIWKSASRVRLERIDGSA 285  
Db 228 -----TYFIIDPETINYIKQS---VMECKEPCSSFEVASAMTW--IARTAFQIPSE 276  
Qy 286 PTEFCRAVDARPAMGVSNYPGLLONMYHNS--TIGEIANESUGATASRLRS---ELD 339  
Db 277 YVKILFGMDMR-----NSFNPLPFGYGNISGTACAVDNVQDLSGLSLRAIMIKS 330  
Qy 340 PASMRQRTGLATYLNHNPKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLGKGPET 399  
Db 331 KVSINDNFKRAVV---KPSELDVMNHE---NVVAFADWSRLGDEVDVFGWNAVSVS 383  
Qy 400 VRRPFPFVESLM--YFM-----PKKPDG 421  
Db 384 ---PVQOQSALAMQNYFLFKPSKNKPDG 409

RESULT 12  
US-09-457-046B-69  
Sequence 69, Application US/09457046B  
Patent No. 6287835  
GENERAL INFORMATION:  
APPLICANT: Croteau, Rodney et al.  
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
FILE REFERENCE: 53679  
CURRENT APPLICATION NUMBER: US/09/457,046B  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69  
LENGTH: 451  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-457-046B-69

Query Match 5.6%; Score 130.5; DB 3; Length 451;  
Best Local Similarity 21.7%; Pred. No. 0.00015;

Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;

Qy 8 DTLQGLPGLLSIYQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK-----61  
Db 29 DQVGTIHTIPLY-----FYDKPSESQGNVVEILKTSLSRVLVHFYPMAGRLRWLPRGR 83  
Qy 62 -----AEGI-----SEGNTGTSFIVPFEDVPRVYVVKLDLDDPSAPTIEGMRKAGYPM 109  
Db 84 FELNCAEGVEFIDAESEK-----LSDFKQFSPTEFENL-----119  
Qy 110 MFDENIIPRKTLPFGPTGDDPKPVILLQNLFIK---GGLILTVNGOHGAMVQDQAVI 168  
Db 120 MPQVNYKNPIETIPL-----FLAQVTKFKCGGISLVNVSIAVD--GQSA-L 164  
Qy 169 RLLS---KACRNDPFTTEEMTAMNLDRTI---VPYLENTYTGPEVDHQ-----211  
Db 165 HLISEWGRGLARGEPL-----TVPELDRKILWAGEP-LPFVSPPKFDHKEFDQPPFLIGE 219  
Qy 212 --IVKADVAGDAVLTVSASWAFFTFSPKAMSELKDA--TKTLDASTKTVSDTDLASA 267  
Db 220 TDNVEERKKKTIVVMLPLSTS-----QLQKRSKANGSKHSDPAKGF-TRYETVVG 269  
Qy 268 FIKWSASRVRLERIDGSAPTFCRAVDARPAM--GVSNYPGLLONMYHNSITGEIANE 325  
Db 270 HWRCACKARGH--SPEQPTALGICIDTRSRMEPPLPRGYFGNATLDVVAASTSGELISN 327  
Qy 326 SIGTASRLRSELDPASMRQRTGLATYLNHNPD-KSNVSLTA-----DADPSTSV 376  
Db 328 ELGFAASLISKAINVTNEYVMIGI-EYLKQKOLKKFQDLHALGSTGPPYGMNLCVV 386  
Qy 377 LSSWAKVGLWDYDFGLGKGPETVRRPPIFEPVESLTMFMP-KKPDGFCFCAALSRLDEMD 435  
Db 387 --SWUTLPMYGLDFWG---KEFYTGCTHDFDGDLSLILPDQEDSGSVILATCLQVAHME 441  
Qy 436 RLK 438  
Db 442 APK 444

RESULT 13  
US-09-457-046B-60  
Sequence 60, Application US/09457046B  
Patent No. 6287835  
GENERAL INFORMATION:  
APPLICANT: Croteau, Rodney et al.  
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
FILE REFERENCE: 53679  
CURRENT APPLICATION NUMBER: US/09/457,046B  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 60  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-457-046B-60

Query Match 5.4%; Score 126.5; DB 3; Length 435;  
Best Local Similarity 20.2%; Pred. No. 0.00036;  
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

Qy 4 KIQLDTLIG-QLPGLLSIYQISLLYP-VSDSSQYPTIVSTFEQGLK-----RFSEAVPW 56  
Db 23 RLQSLDILYCFG---IYVSTIFFYDLITESSE-----VFSENKLSLSLSETLSRFP-L 72  
Qy 57 AGQVKAEGISEGNTGTSFIVPFEDVPRVYVVKLDLDDPSAPTIEGMRKAGYPMAMPDENI 116  
Db 73 AGRIGLSISCNDEGAVFTEARTD---LLLPFLRLNLTDSLSGF-----114  
Qy 117 APRKTLIP-IGPGTGDDPKPVILLQNLFI--KGLLITVNGOHGAMVQDQAVIRLLSK 173  
Db 115 -----LPTLAAGESP-AANPLLSVKVTFFGSGSGVAVSVSHKICDIASLVTFFVK----164

QY 174 ACNDPTEBEEMTAMLDRTKIYVPIYLYNTYIGVEVDHQIVKADVAGDAVLTPVSASWAF 233  
Db 165 ----DWAT-----TTAKGKSNTI-EFAETIYPPPPSHMYEQFSTSDSNIT-----SKYVL 213  
QY 234 --FTFSPKAMSELK-DAATKTLDASTKFVSTDDALSAFTWKS----- 273  
Db 214 KRFVFPKIAELKHAASVSPVTRV-----EAIMSLIWRKARNRSRNLIPROAVMW 269  
QY 274 -----SRVLRERIDGSAPTFCRAVDARPMGVSNYFGLLQNMTHYNSTIGEIA 323  
Db 270 QAMDIRLIRIPSSVAPKDVIGLQSGSLKXDAASSEPEI-----PEIVATPRKNERVNEI 325  
QY 324 NESLGATASRLSELDPASMRQTRGLATYLNHPDKSNVSLTAD-ADPSTSV---MLSS 379  
Db 326 KESLQ-----NTIGQSLLSLMAETVSESTEIDRYIMSS 359  
QY 380 WAKVGLWDYDFGLGLGKPETV---RRPIPEVPSLMYFMPKPDGFCALSLRDEDMDR 436  
Db 360 WCRKPYEVDV--GSGSPVWVGASHTIYDVMGVVLIDSKEGDG-VEAWISLPEEDMSV 416  
QY 437 LKADKEMTKYA 447  
Db 417 FVDDQELLAYA 427

RESULT 14  
US-09-457-046B-68  
; Sequence 68, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679  
; CURRENT APPLICATION NUMBER: US/09/457,046B  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 68  
; LENGTH: 439  
; TYPE: PRT  
; ORGANISM: Catharanthus roseus  
US-09-457-046B-68

Query Match 5.4%; Score 125.5; DB 3; Length 439;  
Best Local Similarity 20.5%; Pred. No. 0.00046;  
Matches 95; Conservative 75; Mismatches 193; Indels 101; Gaps 23;

QY 18 SIY---TQISLLYVPVSDSSQYPIVSTFEQGL-KRPSEAVPWAGQVKAEGISEGNTGTS 73  
Db 39 NIYQTCVSGFFYPENPDGIBISTIREQLQNSLTKLVSYYPFAGKVYKNDYIHCNDDGIE 98  
QY 74 FIVPFDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIAPRKLPIGPGTGDDP 133  
Db 99 FV---EVRICRNDI-----LKTSLSYARDVLPRVT-----VSEDT 136  
QY 134 KPVIQLQNAFKIGGLILTVNGOHGAMDVGQDAVIRLLSK-----ACRNDPTEBEEMTAM 188  
Db 137 TAIVQLS-HFDCGGLAVAFGISH---KVADGGTIASFMKDAASAC-----YL 180  
QY 189 NLDRTKIYVPIYLYNTYIGVEVDHQIVKADVAGDAVLTPVSASWA---FFTFSPKAMSELKD 246  
Db 181 SSSHVPTPLLVSDSIIPRODNIICEQ-----FPTSKNCVEKTFIPPEAIEKLK- 230  
QY 247 AATKTLDASTKFVSTDDALSAFTWKS-----SRVLERIDGSAPTFCRAVDARPMGV 301  
Db 231 --SKAVEFGLEKTRVEVLTAFLSRCATVAGKAANNCGQLPFPVLQAINLRPIEL 288  
QY 302 SNNYPGLLQNMTHYNSTIGEIANESLG-----ATASRLSELDPASMRQTRGLA---- 351  
Db 289 PQNSVGNLVSI-YFSRTIKE--NDYLNKEYTKLVINELAKE-----KQIKNLREKL 339  
QY 352 TYLHNPD-----KSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRPIF 405

Db 340 TYVAQMEEFVKSLEKEDISNFLDID---AYLSDSWCRFPFPDYDF--GWGKPIWV--CLF 392  
QY 406 EPVESLMYFMPKPKDGE---FCAALSLRDEDMRLKADKREWKY 446  
Db 393 QPIYKCVVMDDYFPFGDDYGIARIVSFEQEKSAFEKNEQLLOF 436

RESULT 15  
US-09-457-046B-73  
; Sequence 73, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679  
; CURRENT APPLICATION NUMBER: US/09/457,046B  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 73  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-457-046B-73

Query Match 5.3%; Score 124; DB 3; Length 445;  
Best Local Similarity 19.6%; Pred. No. 0.00068;  
Matches 93; Conservative 79; Mismatches 176; Indels 126; Gaps 23;

QY 20 YTOISLLYVPVSDSSQ---YPTIVSTFEQGL-KRPSEA-VPW--VAGOVKAEG---ISE 67  
Db 37 HTGAVLIYKOPNEDNIHPSMYPFANILIEALSALVPFPYPMAGRLKINGDRVEIDC 96  
QY 68 GNTGTSFIVPFDVPRVVKDLRDDPSAPTIEGMRKAGYPMAFMDENIAPRKLPIGPG 127  
Db 97 NAEALFV---EAESHVLEDFCD--FRPNDE-LHRVMVPTCDYSKGI----- 138  
QY 128 TGPDDPKPVILLQL-NFIKGGILITVNGOHGAMDVG-----QDAV 167  
Db 139 ----SSFPLLMVQLTRFCGGVSGIPAQHHVCDGMAHPEFNNSWARIAKGLLPALPEPVH 194  
QY 168 IRLSKACNDPTEBEEMTAMLDRTKIYVPIYLYNTYIGVEVDHQIVKADVAGDAVLTPV 227  
Db 195 DRYLHLRPRNP-----QIKYSHSQFPPFPVPSLPNELLGK-----T 231  
QY 228 SASWAFPTSPKAMSELKDAATKTLDA--TKFVSTDDALSAFIKWSASRVLERIDGSA 285  
Db 232 NKSQTLFILSREQINTLK-----QKLDLNNYTLSTYEVVAHVRSVSKAR--GLSDHE 285  
QY 286 PTEFCRAVDARPM-----GVSNYPGLLQNMTHYNSTIGEIANESLGATASR----- 333  
Db 286 EIKLIMPVDGRSRINNPSPKPGYCGNVFLAVCTATVGLSCNPLTDTAGKVQEALKGLD 345  
QY 334 ----LRSELDPASMRQTRGLATYLNHPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDF 390  
Db 346 DYLRSIDHTESKP---GLVPYMGSPKTY-----PNVLVNSMGRIPYQAMDF 393  
QY 391 GLGLGKPKETVRPIFPFVESLMY-----FMPKKP-DGEFCAALSLRDEDMRLK 438  
Db 394 GWG-----SPTFFGISNIFDGCFLIPSRDGGSGMTLAINLPSSLSRPF 439

Search completed: January 23, 2005, 19:50:12  
Job time : 33 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 23, 2005, 19:49:13 ; Search time 84 Seconds  
(without alignments)  
1939.780 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAPKIQDLTGLQGLLSIY.....EDMDRLKADKWTKYAQYVG 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:
- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/prodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	13	US-10-074-279-6 Sequence 6, Appli
2	2334	100.0	451	15	US-10-614-954-6 Sequence 6, Appli
3	1860.5	79.7	459	13	US-10-074-279-2 Sequence 2, Appli
4	1860.5	79.7	459	15	US-10-614-954-2 Sequence 2, Appli
5	962.5	41.2	474	13	US-10-074-279-8 Sequence 8, Appli
6	962.5	41.2	474	15	US-10-074-279-8 Sequence 8, Appli
7	187.5	8.0	446	16	US-10-614-954-8 Sequence 178429,
8	176.5	7.6	446	17	US-10-437-963-178429 Sequence 345339
9	175.5	7.5	429	15	US-10-425-115-345339 Sequence 209286
10	175.5	7.4	475	15	US-10-424-599-209286 Sequence 47544, A
11	172.5	7.4	440	17	US-10-425-114-47544 Sequence 222381,
12	172.5	7.4	445	16	US-10-425-115-222381 Sequence 130033,
13	170.5	7.3	436	13	US-10-437-963-130033 Sequence 64, Appli

14	168.5	7.2	446	13	US-10-078-929-52 Sequence 52, Appli
15	168.5	7.2	446	17	US-10-425-115-283768 Sequence 283768,
16	166	7.1	449	16	US-10-437-963-178427 Sequence 178427,
17	165	7.1	468	16	US-10-437-963-146649 Sequence 146649,
18	161	6.9	439	13	US-10-078-929-60 Sequence 60, Appli
19	161	6.9	442	16	US-10-437-963-190353 Sequence 190353,
20	158.5	6.8	1887	16	US-10-437-963-143096 Sequence 143096,
21	158	6.8	466	16	US-10-437-963-179552 Sequence 179552,
22	157.5	6.7	431	16	US-10-437-963-164992 Sequence 164992,
23	156.5	6.7	448	15	US-10-424-599-261757 Sequence 261757,
24	155.5	6.7	394	16	US-10-437-963-200106 Sequence 200106,
25	155	6.6	460	17	US-10-739-930-9224 Sequence 9224, Ap
26	153.5	6.6	460	15	US-10-425-114-46265 Sequence 46265, A
27	152.5	6.5	465	15	US-10-424-599-194573 Sequence 194573,
28	148	6.3	436	17	US-10-425-115-255718 Sequence 255718,
29	147.5	6.3	458	16	US-10-437-963-123563 Sequence 123563,
30	146	6.3	499	17	US-10-425-115-294646 Sequence 294646,
31	146	6.3	504	15	US-10-425-114-57512 Sequence 57512, A
32	144.5	6.2	833	16	US-10-437-963-130430 Sequence 130430,
33	144	6.2	431	13	US-10-078-929-200 Sequence 200, App
34	143	6.1	449	16	US-10-437-963-108868 Sequence 108868,
35	142.5	6.1	457	15	US-10-424-599-277367 Sequence 277367,
36	142	6.1	448	9	US-09-866-572A-56 Sequence 56, Appli
37	142	6.1	448	9	US-09-866-570A-56 Sequence 56, Appli
38	142	6.1	448	14	US-10-166-984-56 Sequence 56, Appli
39	142	6.1	448	15	US-10-166-984-56 Sequence 56, Appli
40	141.5	6.1	436	9	US-09-866-572A-62 Sequence 62, Appli
41	141.5	6.1	436	9	US-09-866-570A-62 Sequence 62, Appli
42	141.5	6.1	436	14	US-10-166-984-62 Sequence 62, Appli
43	141.5	6.1	436	15	US-10-166-984-62 Sequence 62, Appli
44	141.5	6.1	483	16	US-10-437-963-200505 Sequence 200505,
45	140	6.0	447	16	US-10-437-963-168477 Sequence 168477,

ALIGNMENTS

RESULT 1  
US-10-074-279-6  
; Sequence 6, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence1  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Fusarium graminearum  
US-10-074-279-6

Query Match	100.0%	Score 2334;	DB 13;	Length 451;
Best Local Similarity	100.0%	Pred. No. 4.2e-203;		
Matches 451;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1	MAPKIQDLTGLQGLLSIYQTISLLYPVSDSQYPTIVSTFPGGLKRFSEAVPWAGQV	60	
Db	1	MAPKIQDLTGLQGLLSIYQTISLLYPVSDSQYPTIVSTFPGGLKRFSEAVPWAGQV	60	
Qy	61	KABGISEGNTGTSFIYPPFDVPRVVVKDLRDDPSATIEGMRKAGYPMAFDENIAPRK	120	

Db 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAFTIEGMRKAGYPMAMFDENIIAPRK 120  
Qy 121 TLPFGTGPDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNDPF 180  
Db 121 TLPFGTGPDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNDPF 180  
Qy 181 TEEMTAMNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKA 240  
Db 181 TEEMTAMNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKA 240  
Qy 241 MSELKDAATKTLDASTKFVSTDDALSFAFTWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300  
Db 241 MSELKDAATKTLDASTKFVSTDDALSFAFTWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300  
Qy 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLRSELDPASMRQTRGLATYLLHNPDK 360  
Db 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLRSELDPASMRQTRGLATYLLHNPDK 360  
Qy 421 GEFCAALSRLDEDMDLKADKWKTKYAQYVG 451  
Db 421 GEFCAALSRLDEDMDLKADKWKTKYAQYVG 451

## RESULT 2

US-10-614-954-6  
; Sequence 6, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; PRIOR FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Fusarium graminearum  
US-10-614-954-6

Query Match 100.0%; Score 2334; DB 15; Length 451;  
Best Local Similarity 100.0%; Pred. No. 4.2e-203;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAFKIQLDTLGOLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
Db 1 MAFKIQLDTLGOLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60  
Qy 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAFTIEGMRKAGYPMAMFDENIIAPRK 120  
Db 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAFTIEGMRKAGYPMAMFDENIIAPRK 120  
Qy 121 TLPFGTGPDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNDPF 180  
Db 121 TLPFGTGPDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNDPF 180  
Qy 181 TEEMTAMNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKA 240  
Db 181 TEEMTAMNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKA 240

Qy 241 MSELKDAATKTLDASTKFVSTDDALSFAFTWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300  
Db 241 MSELKDAATKTLDASTKFVSTDDALSFAFTWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300  
Qy 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLRSELDPASMRQTRGLATYLLHNPDK 360  
Db 301 VSNYPGLLQNMTHNSTTIGETANESLGATASRLRSELDPASMRQTRGLATYLLHNPDK 360  
Qy 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPD 420  
Qy 421 GEFCAALSRLDEDMDLKADKWKTKYAQYVG 451  
Db 421 GEFCAALSRLDEDMDLKADKWKTKYAQYVG 451

## RESULT 3

US-10-074-279-2  
; Sequence 2, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR FILING DATE: US/09/538,414  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Fusarium sporotrichioides  
US-10-074-279-2

Query Match 79.7%; Score 1860.5; DB 13; Length 459;  
Best Local Similarity 77.6%; Pred. No. 4.8e-160;  
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

Qy 2 AFKIQLDTLGOLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 61  
Db 11 SFDIELDIITGOOPPLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRLSQTFFPWAGQV 70  
Qy 62 ARGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAFTIEGMRKAGYPMAMFDENIIAPRK 121  
Db 71 TEGISEGNTGTSKIIPYEETPLRVKDLRDDSSAFTIEGLRKAGPPELFDENVVAPRK 130  
Qy 122 LPIPGTGPDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNDPF 181  
Db 131 LAIGPENGNDPKPVILLQNLFIKGGILITVNGQHGANDMGQDAVIRLLSKACRNEST 190  
Qy 182 EREMTAMNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKAM 241  
Db 191 EBEISANNLDRTIIVPLENTTIGPEVDHQIVKADVAGGDVLTVPVSASWAFFTFSPKAL 249  
Qy 242 SELKDAATKTLDASTKFVSTDDALSFAFTWKSASRVRLERIDGSAPTEFCRAVDARPAMG 301  
Db 250 SELKDAATKTLDASSKFVSTDDALSFAFTWQSTSRVRLARLDASTTEFCRAVDMRGPVG 309  
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Qy 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIPEPVESLMYFMPKKPDG 421



Db 370 SVSLTADANPSSIMLSWAKVCCWEYDFGFLGKPESVRRPPEFESLMYFMPKPKPDG 429  
QY 422 EFCAALSLRDEDMRLKADKEWTKYAYVG 451  
Db 430 EFTASISLRDEDMERLKADKEWTKYAKYIG 459

RESULT 4  
US-10-614-954-2  
; Sequence 2, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; PRIOR FILING DATE: 2003-07-07  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Fusarium sporotrichioides  
US-10-614-954-2

Query Match 79.7%; Score 1860.5; DB 15; Length 459;  
Best Local Similarity 77.6%; Pred. No. 4.8e-160;  
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

QY 2 AFKIQDITGQLPGLLSIYTIQISLVPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVK 61  
Db 11 SFDIELDIIGQQPPLLSIYTIQISLVPVSDSSQYPTIVSTFEGLKRLSQTFFWVAGQVK 70  
QY 62 AGISGNTGTSITVPFEDVPRVVKDLRDDPSAPTIEGRKAGYPWAMFENIIAPRKT 121  
Db 71 TEGISEGNTGTSKIIYEETPRVLVVKDLRDDSSAPTIEGLRKAGPPEMDENNVAPRKT 130  
QY 122 LPTGPGTDPDPKPVILLQNLNFIKGLILTVNGHGMVGDVIRLLSKACRNDPPT 181  
Db 131 LAIPGNGNDPKPVILLQNLNFIKGLILTVNGHGMVGDVIRLLSKACRNEST 190  
QY 182 EEMTAMNLDKRTIVPYLENTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFPTFSPKAM 241  
Db 191 EEEISAMNLDKRTIVPYLENTTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFPTFSPKAL 249  
QY 242 SELKDAATKTLDASTFVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPA 301  
Db 250 SELKDAATKTLDASTFVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPA 309  
QY 302 SNNYPGLLQNTVHNSTIGEIANESLGATASRLRSELDPA--SMRQRTGLATYLNH 361  
Db 310 SSTYPGLLQNTVHNSTIGEIANESLGATASRLRSELDPA--SMRQRTGLATYLNH 369  
QY 362 NVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPKETVRRPIPEFVESLMYFMPKPKPDG 421  
Db 370 SVSLTADANPSSIMLSWAKVCCWEYDFGFLGKPESVRRPPEFESLMYFMPKPKPDG 429

QY 422 EFCAALSLRDEDMRLKADKEWTKYAYVG 451  
Db 430 EFTASISLRDEDMERLKADKEWTKYAKYIG 459

RESULT 5  
US-10-074-279-8  
; Sequence 8, Application US/10074279

; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-074-279-8

Query Match 41.2%; Score 962.5; DB 13; Length 474;  
Best Local Similarity 44.4%; Pred. No. 2.2e-78;  
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITLQGLPGLLSIYTIQISLVPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVKAEGI 65  
Db 22 QLDITLQGLPGLLSIYTIQISLVPVSDSSQYPTIVSTFEGLKRFSEAVPWVAGQVKAEGI 81  
QY 66 SEGNTGTSITVPFEDVPRVVKDLRDDPSAPTIEGRKAGYPWAMFENIIAPRKT-PI 124  
Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSEKADFFIYMLDEKTFAPCMTINPP 140  
QY 125 GPGTG-PDDPKPVILLQNLNFIKGLILTVNGHGMVGDVIRLLSKACRNDPTEE 183  
Db 141 GMTIGNAAKSGPVFAVQANFISGGLVLTIVGQHNINDITGQESIIINLLKSKCHQKPFSD 200  
QY 184 EMTAMNLDKRTIVPYLENTTIGPEVD--HQIVKA--DVAGGDAVLTVPVS--ASWAFPTFSP 238  
Db 201 ELLIGNIDSKSIPLFDE-TWEPDITLVHEIVETSNTSGEEKEQSCSSNSTWAYVEFSA 259  
QY 239 KAWSELKDAATKTLDASTFVSTDDALSAPFWKSASRVRLERIDGSAPTEFCRAVDARPA 298  
Db 260 ISLQNLRIILAMQTCISGTFVSTDDITVAFIWKSVSRARLSRLKPKETKSNLGRADVVRK 319  
QY 299 MGVSNNYPGLLQNTVHNSTIGEIANESLGATASRLRSELDPA--SMRQRTGLATYLNH 356  
Db 320 LGLPETYPGLLQNTVHNSTIGEIANESLGATASRLRSELDPA--SMRQRTGLATYLNH 379  
QY 357 NPDKSNVSLTADADPSTVMSLSSWAKVGLWDYDFGLGKPKETVRRPIPEFVESLMYFMP 416  
Db 380 CPDKTKVSIQPDITLDSGIMVSSWAKVGLYDVFNLGLGKPKSVRRPRTISLESILYFMP 439  
QY 417 KXPDGFECAALSRLRDEDMRLKADKEWTKYAYVG 451  
Db 440 RSSRGEVVALCLRDKWECLNADKEWTKYATHIG 474

RESULT 6  
US-10-614-954-8  
; Sequence 8, Application US/10614954  
; Publication No. US20040034884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods

```

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-8

Query Match      41.2%; Score 962.5; DB 15; Length 474;
Best Local Similarity 44.4%; Pred. No. 2.2e-78;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITGQLPGLLSIYQISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQVKAEGI 65
DB 22 QLDILGQPSLYKLYQICSIYRVPDPSAHDHVLNLTGLETAKNFOWLAGNVVNEGA 81
QY 66 SEGNTGTSFTVPEDVPRVVVKDLRDDPSAPTIETGMRKAGYPMPMPDENIAPKTL-PI 124
DB 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFPYMLDEKTFAPCMTINPP 140
QY 125 GPOTG-PDDPKPVILLQOLPIKGLLITVNGQHGAMDMVQDAVIRLLSKACRNDPFTEE 183
DB 141 GNTIGMAKSGPFAVQANFISGLGLVLTIVGQHNIMDITGOSSIINLLNKSCHQKPFSE 200
QY 184 EMTANLDRKTIYPYLENTYIGPEVD--HOIVKA--DVAGGDVAVLTPVS-ASWAFFTFSP 238
DB 201 ELIGNIDKSKSLPLFDE-TWEDPTLVHEIVTSRNTSGEEKESQSSNTHWYVEFSA 259
QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFWKSASRVRLERIDGSAFTFCRAVDARPA 298
DB 260 ISLQNLRIILAMQICTSGTKFVSTDDIVTAFIWKSVSRARLSRLKPKETKNLGRAVDVRKR 319
QY 299 MGVSNNYPGLLQNTWYTHNSTIGIANESLGATASRLSELDPDPA--SMQRTGRLATYLN 356
DB 320 LGLPETYGLLVNNTFTGSLKSLDHSKSLVILASQIRKLDPKVDFLANTCALATLLSR 379
QY 357 NPDKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLGLGKPEVRRPPIPEPVESLMYFMP 416
DB 380 CPDKTKVSIQPIDTSLGIVSSWAKVSLYDVDFNLGLGKPKSVRRPRFTISLESIFYFMP 439
QY 417 KPDGFCFCAALSURDEMDRLKADKWKTKYQVVG 451
DB 440 RSSRGMVVALCLRDKDWECNLADKWTNYATHIG 474

RESULT 7
US-10-437-963-178429
; Sequence 178429, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178429
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Oryza sativa
;

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345339
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1.pap
; US-10-425-115-345339

Query Match      7.6%; Score 176.5; DB 17; Length 446;
Best Local Similarity 24.4%; Pred. No. 5.8e-07;
Matches 109; Conservative 58; Mismatches 218; Indels 61; Gaps 19;

QY 13 LPGLLSIYTCISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQVKAEGI-----ISEG 68
DB 40 LPYITFYNQKLLLYRA--APDFPDVARNMTAALADALRVFFLAGIRIQDDGGALAVEG 97
QY 69 NTGTSFTVPFE-DVPRVVVKDLRDDPSAPTIETGMRKAGYPMPMPDENIAPKTLPIGPG 127
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; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345339
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1.pap
; US-10-425-115-345339

Query Match      7.6%; Score 176.5; DB 17; Length 446;
Best Local Similarity 24.4%; Pred. No. 5.8e-07;
Matches 109; Conservative 58; Mismatches 218; Indels 61; Gaps 19;

QY 13 LPGLLSIYTCISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQVKAEGI-----ISEG 68
DB 40 LPYITFYNQKLLLYRA--APDFPDVARNMTAALADALRVFFLAGIRIQDDGGALAVEG 97
QY 69 NTGTSFTVPFE-DVPRVVVKDLRDDPSAPTIETGMRKAGYPMPMPDENIAPKTLPIGPG 127

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/437963
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-10-614-954-8

Query Match      41.2%; Score 962.5; DB 15; Length 474;
Best Local Similarity 44.4%; Pred. No. 2.2e-78;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITGQLPGLLSIYQISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQVKAEGI 65
DB 22 QLDILGQPSLYKLYQICSIYRVPDPSAHDHVLNLTGLETAKNFOWLAGNVVNEGA 81
QY 66 SEGNTGTSFTVPEDVPRVVVKDLRDDPSAPTIETGMRKAGYPMPMPDENIAPKTL-PI 124
DB 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFPYMLDEKTFAPCMTINPP 140
QY 125 GPOTG-PDDPKPVILLQOLPIKGLLITVNGQHGAMDMVQDAVIRLLSKACRNDPFTEE 183
DB 141 GNTIGMAKSGPFAVQANFISGLGLVLTIVGQHNIMDITGOSSIINLLNKSCHQKPFSE 200
QY 184 EMTANLDRKTIYPYLENTYIGPEVD--HOIVKA--DVAGGDVAVLTPVS-ASWAFFTFSP 238
DB 201 ELIGNIDKSKSLPLFDE-TWEDPTLVHEIVTSRNTSGEEKESQSSNTHWYVEFSA 259
QY 239 KAMSELKDAATKTLDASTKFSVSTDDALSAPFWKSASRVRLERIDGSAFTFCRAVDARPA 298
DB 260 ISLQNLRIILAMQICTSGTKFVSTDDIVTAFIWKSVSRARLSRLKPKETKNLGRAVDVRKR 319
QY 299 MGVSNNYPGLLQNTWYTHNSTIGIANESLGATASRLSELDPDPA--SMQRTGRLATYLN 356
DB 320 LGLPETYGLLVNNTFTGSLKSLDHSKSLVILASQIRKLDPKVDFLANTCALATLLSR 379
QY 357 NPDKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLGLGKPEVRRPPIPEPVESLMYFMP 416
DB 380 CPDKTKVSIQPIDTSLGIVSSWAKVSLYDVDFNLGLGKPKSVRRPRFTISLESIFYFMP 439
QY 417 KPDGFCFCAALSURDEMDRLKADKWKTKYQVVG 451
DB 440 RSSRGMVVALCLRDKDWECNLADKWTNYATHIG 474

RESULT 7
US-10-437-963-178429
; Sequence 178429, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178429
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Oryza sativa
;

; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345339
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1.pap
; US-10-425-115-345339

Query Match      7.6%; Score 176.5; DB 17; Length 446;
Best Local Similarity 24.4%; Pred. No. 5.8e-07;
Matches 109; Conservative 58; Mismatches 218; Indels 61; Gaps 19;

QY 13 LPGLLSIYTCISLLYPVSDSSOYPTIVSTFEQGLKRFSEAVPWAGQVKAEGI-----ISEG 68
DB 40 LPYITFYNQKLLLYRA--APDFPDVARNMTAALADALRVFFLAGIRIQDDGGALAVEG 97
QY 69 NTGTSFTVPFE-DVPRVVVKDLRDDPSAPTIETGMRKAGYPMPMPDENIAPKTLPIGPG 127
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RESULT 12  
US-10-437-963-130033  
; Sequence 130033, Application US/10437963  
; Publication No. US20040123342A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude

RESULT 13  
US-10-078-929-64  
Sequence 64, Application US/10078929  
Publication No. US20020152497A1  
GENERAL INFORMATION:  
APPLICANT: Rafaleski, Antoni  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Sakai, Hajime  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Odell, Joan I.  
APPLICANT: Meyers, Blake  
APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; FILE REFERENCE: BB1357 US NA  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 64  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-078-929-64

Query Match 7.3%; Score 170.5; DB 13; Length 436;  
Best Local Similarity 20.4%; Pred. No. 2e-06;  
Matches 84; Conservative 61; Mismatches 158; Indels 109; Gaps 15;  
QY 56 VAGQVKAEGISEGN-----TGTSFIVPFEDVPRVVVKLRDDPSAPTIEGMRKAGYPMA 109  
DB 78 LAGRLGREG--EGRLQIDCNGSGALFVLARAPDVAGEDLFGSGYFSPSE-IRRMFVPPA 134  
QY 110 MPDENIIAPRKTLPICPGTGPDPKPVILLQLNFIK-GGLILTVNGQHGAMVGDVAVI 168  
DB 135 -----PSG-----DPPCHAMFQVTLKCGGVVLGTGHHVTMDGMAFHFI 176  
QY 169 RL-----LSKACNRDPFTEEMTAMNLDRTKTIIVPLENTYIGPEVDHQIVKADVAG 219  
DB 177 QTWGLAGLSLEACSPFPFHDRTLLRARSPPR-----PEFEHPVYSAYLN 224  
QY 220 GDVAVLTPVSASWAFPTSPKMSSELKDAATKTLIDASTKTFVSTDDALSFIWK----- 271  
DB 225 G-----APRPFTVTVSVSQKLLADIKSRCAFG-----VSTYGAVTAHLWRCMCVARGL 273  
QY 272 ---SASRVRL-----BRIDGSAFTEFCRAVDARPMGVSNVYPLLQNNMTHNSTIGETA 323  
DB 274 AFGSDTLRLVPANIRHLRQLPRQFNGNAIVRDLTVTK-----VGDLV 317  
QY 324 NESLIGATASRLSELDPSAMRQRTGLATYLHNNDKSNVSLTADADPSTSVMLSSWAKV 383  
DB 318 SQPLGYVAUTIRKAVDHDV-DATRSVIDYLEVESEKGSQAARGQLMPESDLWVSVLGM 376  
QY 384 GLWDYDFGLGLGKPKETVRRPIFEVPSLMYFMPKPDGFECAALSURDEMD 435  
DB 377 PMYDADFGWGAAPR-----FVAPAQMGFGSGTAVYVTKGADRD 412

RESULT 14  
US-10-078-929-52  
; Sequence 52, Application US/10078929  
; Publication No. US20020152497A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime

; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; FILE REFERENCE: BB1357 US NA  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 52  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-078-929-52

Query Match 7.2%; Score 168.5; DB 13; Length 446;  
Best Local Similarity 21.8%; Pred. No. 3.1e-06;  
Matches 98; Conservative 63; Mismatches 177; Indels 111; Gaps 21;  
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DB 24 NSGPDLVVPRFTPSYVF-FRREDADGNLDAGADGSGFFDGMRRRALAALVFFYPMAGR 82  
QY 110 -----MFDE-----NIAP-----RKTLPICGTGPDPPKPV 136  
DB 83 LARDEDGRVEIDCAGGVLFQEADAPDATIDYFGDFAPTMELKRLIPTVDFDIDSSFPL 142  
QY 137 ILLQLNFIK-GGLILTVNGQHGAMVGDVAVIRLLSKACNRDPFTEEMTAMNLDRTI 195  
DB 143 LVLQVTHFKCGGVAIGVGMQHHVADGFSGLHFINSWADLCRGVPI-----AV 189  
QY 196 VPLENTYIG-----PEVDHQIVKADVA-GGDVAVLTPVSA-----SWAFPTSPKAM 241  
DB 190 MPFIDRSLRLARDPPTPAYPHIEYQAPAMLSEPPQAALTSKPATPTAVAFKLSRAEL 249  
QY 242 SELKDAATKTLIDASTKTFVSTDDALSAFIWKASRVRLERIDGSAFTEFCRAVDARPMGV 301  
DB 250 VRLR-SQVPAEGAPFP-STYAVLAHVRWCASLAR--GLPADQPTKLYCATDGRQL-- 303  
QY 302 SNNYP----GLLQNNMTHNSTIGETANESLGAT--ASRLRSELDPSAMRQRTGLATYLH 355  
DB 304 ---QPPLPSGFGNVIPTATPLANAGTVTAGVAEGASVIAQALDRMD-DGYCRSALDYLE 359  
QY 356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPKETVRRPIFE-----PVES 410  
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; Sequence 283768, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 283768  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_21897C.1.pep  
US-10-425-115-283768  
  
Query Match 7.2%; Score 168.5; DB 17; Length 446;  
Best Local Similarity 21.8%; Pred. No. 3.le-06;  
Matches 98; Conservative 63; Mismatches 177; Indels 111; Gaps 21;  
  
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Db 83 LARDEGRVEIDCAGGVLFQEADAPDATIDYFGDFAPTMLKRLIPTVDFDDISSFPL 142  
  
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QY 196 VPYLENTYIG-----PEVDHQIVKADVA-GGDAVLTPVSA-----SWAFFTFSPKAM 241  
Db 190 MPFIDRSLRLARDPPPTPAYPHIEYQAPAPMLSEPPQALTSKEATPTTAVAIKLSRAEL 249  
  
QY 242 SELKDAATKTLDASTKFSVSTDDALSAFIWKASRVRLERIDGSAPTEFCRAVDARPAAGV 301  
Db 250 VRLR-SQVPARECAPRF-STYAVLAHVWRCSLAR--GLPADQPTKLYCATDGRQL-- 303  
  
QY 302 SNNYP-----GLLQNMTHNSTIGEIANESIGAT--ASRLRSELDPASMEQRTGLATYLH 355  
Db 304 ---QPPLPEGYFGNVITATPLANAGTVTAGVAEGASVIOAALDRMD-DGYCRSALDYLE 359  
  
QY 356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRRPIFE-----PVES 410  
Db 360 LQPDLSALVRGAHTFCPNLGLTSWVRLPIHDADFCWG-----RPVFMGPGGIAYEG 411  
  
QY 411 LMYFMKP-KPDGEFCAALSDEDMRLK 438  
Db 412 LAFVLPANRSGSLSLVAISLQAEHMEKFR 440

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Job time : 87 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 24, 2005, 01:40:16 ; Search time 6057 Seconds  
(without alignments)  
3521.158 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAFKIQDTLQGLGLSIY.....EDMDRLKADKEWTKYQYVG 451

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=GenEmbl -QFT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10614954 @CN 1 1 3731 @runat 19012005 171526 25178 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

RESULT 1	BD247864	1356 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD247864	Transgenic plant and methods.			
DEFINITION	BD247864				
ACCESSION	BD247864.1	GI:33057634			
VERSION	JP 2002540787-A/4.				
KEYWORDS	Gibberella zeae				
SOURCE	Gibberella zeae				
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.				
REFERENCE	1 (bases 1 to 1356)				
AUTHORS	Hohn,T.M., Peters,C., Salmeron,J.M., Janet, Reed,N. and Dawson,J.L.				
TITLE	Transgenic plant and methods				
JOURNAL	Patent: JP 2002540787-A 4 03-DEC-2002;				
COMMENT	SYNGENTA PARTICIPATIONS AG				
	OS Fusarium graminearum				
	PN JP 2002540787-A/4				
	PD 03-DEC-2002				
	PF 29-MAR-2000 JP 2000609553				
	PR 31-MAR-1999 US 09/282995,11-FEB-2000 US 09/502852 PI				
	THOMAS M HOHN, CHERYL PETERS, JOHN MANUEL SALMERON, JANET PI N				
	REED, JOHN L DAWSON				
	PC C12N15/09, A01H5/00, C12N1/15, C12N5/10// (C12N1/15, C12R1:645), PC				
	(C12N5/10, C12R1:91), C12N15/00, C12N5/00, C12N5/00, C12N5/00, C12R1:91) CC				
	Transgenic plant and methods				
	PH Key Location/Qualifiers				
	FT source 1. .1356				

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	1356	6	BD247864 Transgeni
2	2334	100.0	1356	6	AR193433 Sequence
3	2334	100.0	1356	6	AR430218 Sequence
4	2314	99.1	1605	6	E31785 Trichothec



FT /organism='Fusarium graminearum'.  
 source Location/Qualifiers  
 1. .1356  
 /organism="Gibberella zeae"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:5518"

## ORIGIN

## Alignment Scores:

Pred. No.: 3,42e-167 Length: 1356  
 Score: 2334.00 Matches: 451  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-614-954-6 (1-451) x BD247864 (1-1356)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20  
 DB 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCGAGCTCCCTTTTCGATCTAC 60  
 QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40  
 DB 61 ACCCAATCAGTCTCTCTACCCGCTCTCTGATTCCTCAATATCCCACTATTGTGACG 120  
 QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60  
 DB 121 ACCTTCGAGCAGGCTTTAAGCGCTTCTCGAAGCGCTCCCATGGGTCCGACGCCAGGTC 180  
 QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
 DB 181 AAGCCGAGGGCAATTAGCGAGGGAACACAGNACTTCCTTTATCGTCCCTTTGAGGAC 240  
 QY 81 ValProArgValValLysAspLeuArgAspProSerAlaProThrIleGluGly 100  
 DB 241 GTTCCTCGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300  
 QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLys 120  
 DB 301 ATGAGAAAGCGGGATACCTATGGGATGTTGACGAGAACATCATCGGCCCAAGAG 360  
 QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln 140  
 DB 361 ACCTTACCTATTGGACCTGGTACTGGTCCGACGACCCAAAGCCTGTAATCTATTGCGAG 420  
 QY 141 LeuAsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
 DB 421 CTCAACTTCATCAAGGCGGACTCATCTCCTCAACGACGACGACGATGGTATGGAT 480  
 QY 161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180  
 DB 481 ATGGTAGGCCAAGATCGGATGCTCGTCTACTCTCCAGGCGTCCGTAACGCCCATTC 540  
 QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200  
 DB 541 ACCGAGAGGAATATGCGGCCCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTGA 600  
 QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220  
 DB 601 AACTATACGATGGCCCGGAGTAGATCATCAGATTGTCAAGCTGATGTAGTGTGGT 660  
 QY 221 AspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAla 240  
 DB 661 GAGCGTGTCTCAGCCCGGTGAGTGCNAGCTGGCGTCTTCACATTCAGCCCCAAGGCC 720  
 QY 241 MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260  
 DB 721 ATGTCAGAGCTCAAGGATGCTGCTTACCAAGACTCTTGACGCATCAACAAAGTTCTGTCG 780  
 QY 261 ThrAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280  
 DB 781 ACTGACGATGCTCTTCGCGGTTTCATCTGGAATCGGCCCTCTCGCGTGTCTCGAAGA 840

QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
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 QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320  
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 QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340  
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 QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440  
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## RESULT 2

LOCUS AR193433 1356 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 5 from patent US 6346655.  
 ACCESSION AR193433  
 VERSION AR193433.1 GI:20239398  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1356)  
 AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.  
 TITLE Trichothecene-Resistant transgenic plants  
 JOURNAL Patent: US 6346655-A 5 12-FEB-2002;  
 FEATURES  
 Location/Qualifiers  
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## ORIGIN

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-614-954-6 (1-451) x AR193433 (1-1356)

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Qy 61 LysAlaGluGlyIleSerGluGlyAanThrGlyThrSerPheIleValProPheGluAsp 80
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Db 541 ACCGAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGCAGATAGTCTTACCTTGAA 600
Qy 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 220
Db 601 AACTATACGATTGGCCCGGAGGTAGATCATCATGATGTCAAAGCTGATAGTGTGTGT 660
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Qy 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300
Db 841 ATCGATGGCTCTGCACCTACCGAGTCTCGCGGTGCTGTGATGCTCGACCGGCATGGGT 900
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Qy 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400
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Qy 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
Db 1261 GCGGAGTTCTGTGCGCGCTTTCTCTGAGGATGAGGATATGACCGATGAGCGGAT 1320
Qy 441 LysGluTrpThrLysTyrAlaGlnTyrValGly 451
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RESULT 3
LOCUS AR430218 1356 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6646184.
ACCESSION AR430218
VERSION AR430218.1 GI:40190948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmeron,J.
TITLE Trichothecene-resistant transgenic plants
JOURNAL Patent: US 6646184-A 5 11-NOV-2003;
FEATURES
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Alignment Scores:
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Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-614-954-6 (1-451) x AR430218 (1-1356)
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Db 61 ACCCAATCAGTCTCTCTACCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120
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Db 1141 GCCAAGTGGGACTCTGGGATACGACTTTGGCTCGGACTGGGTAAAGCCCGAGCTGTG 1200  
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## RESULT 4

E31785  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

E31785  
Trichothecene 3-O-acetyltransferase gene.  
E31785  
E31785.1 GI:13018619  
JP 2000032985-A/1.  
Gibberella zeae  
Gibberella zeae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1605 bp DNA linear PAT 18-JUN-2001

## REFERENCE

1 (bases 1 to 1605)

Isamu, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.

Trichothecene 3-O-acetyltransferase gene

Patent: JP 2000032985-A 1 02-FEB-2000;

RIKAGAKU KENKYUSHO, ISAMU YAMAGUCHI

OS Fusarium graminearum

PN JP 2000032985-A/1

PD 02-FEB-2000

PP 15-JUL-1998 JP 1998200280

PR ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI

KOSHINO, PI KATSUMI YONEYAMA

PC C12N15/09, A01H5/00, A01N63/00, C12N1/21, C12N5/10, C12N9/10// PC

(C12N15/09, C12R1/77), (C12N1/21, C12R1/19), (C12N5/10, C12R1/91), PC

C12N15/00,

PC C12N5/00, C12N15/00, C12R1/77), (C12N5/00, C12R1/91) CC

FH Key Location/Qualifiers

FT CDS 135..1487.

Location/Qualifiers

1..1605

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## ORIGIN

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Query Match: 99.14% Indels: 0  
DB: 6 Gaps: 0

US-10-614-954-6 (1-451) x E31785 (1-1605)

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LOCUS  
DEFINITION  
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complete cds.  
AB000874  
ACCESSION  
VERSION  
AB000874.1 GI:2804249  
KEYWORDS  
trichothecene 3-O-acetyltransferase.  
SOURCE  
Gibberella zeae  
ORGANISM  
Gibberella zeae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
REFERENCE  
1 (sites)  
Kimura M., Kaneko I., Komiyama M., Takatsuki A., Koshino H.,  
Yoneyama K. and Yamaguchi I.  
TITLE  
Trichothecene 3-O-acetyltransferase protects both the producing  
organism and transformed yeast from related mycotoxins. Cloning and  
characterization of trl101  
J. Biol. Chem. 273 (3), 1654-1661 (1998)

98104153  
9430709  
REFERENCE  
2 (bases 1 to 1605)  
AUTHORS  
Kimura M.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical  
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;  
Hiroseawa 2-1, Wako, Saitama 351-01, Japan  
(E-mail:mkimura@postman.riken.go.jp, Tel:81-048-467-9518,  
Fax:81-048-462-4676)  
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Best Local Similarity: 99.11% Mismatches: 4  
Query Match: 99.14% Indels: 0  
DB: 8 Gaps: 0  
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Db 195 ACCCAATCAGTCTCCTTACCCCGTCTCTGATCCCTCTCAATATATCCCACTATTGTGACG 254  
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Qy 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
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 QY 441 LysGluTrpThrLysTyrAlaGlnTyrValGly 451  
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 3-O-acetyltransferase, partial and complete cds.  
 ACCESSION  
 AB009607  
 VERSION  
 AB009607.1 GI:3252781  
 KEYWORDS  
 Tril01; trichothecene 3-O-acetyltransferase; UTP-ammonia ligase.  
 SOURCE  
 Gibberella zeae

ORGANISM  
 Gibberella zeae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 REFERENCE  
 1 Kimura,M., Shingu,Y., Yoneyama,K. and Yamaguchi,I.  
 Features of Tril01, the trichothecene 3-O-acetyltransferase gene,  
 related to the self-defense mechanism in Fusarium graminearum  
 Biosci. Biotechnol. Biochem. 62 (5), 1033-1036 (1998)  
 JOURNAL  
 MEDLINE  
 PUBMED  
 98312047  
 9648241  
 REFERENCE  
 2 (bases 1 to 3003)  
 Kimura,M.  
 Direct Submission  
 Submitted (06-DEC-1997) Makoto Kimura, The Institute of Physical  
 and Chemical Research (RIKEN), Microbial Toxicology Laboratory;  
 Hirosawa 2-1, Wako, Saitama 351-0198, Japan  
 (E-mail:mkimura@postman.riken.go.jp, Tel:81-48-467-9518,  
 Fax:81-48-462-4676)  
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 Alignment Scores:  
 Pred. No.: 3,23e-165 Length: 3003  
 Score: 2314.00 Matches: 447  
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 Best Local Similarity: 99.11% Mismatches: 4  
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## CDS

## ORIGIN

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 Score: 2314.00 Matches: 447  
 Percent Similarity: 99.11% Conservative: 0  
 Best Local Similarity: 99.11% Mismatches: 4  
 Query Match: 99.14% Indels: 0  
 DB: 8 Gaps: 0

US-10-614-954-6 (1-451) x AB011417 (1-8646)

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 ACCESSION  
 AF212605  
 VERSION  
 AF212605.1  
 GI:12003706  
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 SOURCE  
 ORGANISM  
 Gibberella zeae  
 Gibberella zeae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Gibberella.  
 REFERENCE  
 1 (bases 1 to 1336)



AUTHORS	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.	QY	141	LeuAenPheIleIysGlyGlyLeuLeuThrValAsnGlyClnHisGlyAlaMetAsp	150
TITLE	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab	Db	423	CTCAACTTCATCAAGGGCGGACTCATCTCTCACTGTCAAGGACAGCAGCGTGTATGGAT	482
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)	QY	161	MetValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPhe	180
MEDLINE	20345085	Db	483	ATGGTAGGCCAAGATCGGTGATCCGTCTCTCCAGGCGTCCGTACGACCCCATTC	542
REFERENCE	10869425	QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProLysLeuGlu	200
AUTHORS	O'Donnell, K.	Db	543	ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGCAGATAGTCTCTTACCTTGA	602
TITLE	Direct Submission	QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly	220
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research.	Db	603	AACTATACGATTGGCCCCGAGGTAGATCATCATGATTGTCAAAGCTGATGTAGTGGTGT	662
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source	Location/Qualifiers	Db	663	GACGCTGTTCTCAGCCCGGTGAGTGCAGCTGGCGGCTTTCTTCAATTCAGCCCCAAGGCC	722
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ORIGIN	US-10-614-954-6 (1-451) x AF212605 (1-1336)	QY	361	SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp	380
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Pred. No.:	2.5e-164	QY	381	AlaLysValGlyLeuThrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal	400
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Best Local Similarity:	100.00%	Db	1203	AGACGCCCAATCTTTGAGCTGTGAGAGCTTGATGATCTTTATGCCCAAGAACCTGAT	1262
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		KEYWORDS			
		SOURCE			

ORGANISM	Gibberella zeae	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
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AUTHORS	1 (bases 1 to 1336)	QY	141	LeuAsnPheIleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160
TITLE	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab	Db	423	CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGGACGACGCTGTATGGAT 482
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)	QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180
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PUBMED	10869425	QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200
REFERENCE	2 (bases 1 to 1336)	Db	543	ACCGAAGAGGAATGACGCCCATGAACTCGATCGCAACGATAGTTCTTACCTTGAA 602
AUTHORS	O'Donnell, K.	QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 220
TITLE	Direct Submission	Db	603	AACTATACGATTGGCCCGGAGGTAGATCATCATGTTGTCAAAGCTGATGTAGCTGGT 662
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1915 N. University St., Peoria, IL 61604, USA	QY	221	AspAlaValLeuThrProValSerAlaSerTropAlaPhePheThrPheSerProLysAla 240
FEATURES	Location/Qualifiers	Db	663	GACGCTGTTCTCACGCCGTCAGTCAAGCTGGGGTCTTCAATTCAGCCCCAAGGCC 722
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	<3. >1336	Db	843	ATCGATGGCTCTGCACTACCGAGTCTCGCGTGTCTGTTGATGCTCGACCGGCAATGGT 902
	/product="trichothecene 3-O-acetyltransferase"	QY	301	ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320
	3. >1336	Db	903	GTCTCGAACAACTACCCAGGCTCTTCTCAAAACATGACCTACCACTCGACCATCGGC 962
	/codon_start=1	QY	321	GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340
	/product="trichothecene 3-O-acetyltransferase"	Db	963	GAATTCGCCCAACAGTCACTCGCGCAACAGCATCACGCTTCGTTCAGAACCTCGACCC 1022
	/protein_id="AAG43715.1"	QY	341	AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360
	/db_xref="GI:12003713"	Db	1023	GGAGCATCGCCAGCAACAGAGTCTCGCGAGTACCTCGACCAACACCCGACAAAG 1082
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	ORIGIN	Db	1083	TCCAACGTTATCCTGACGGCTGATCGGACCCCATCTACGAGGTCATGCTGAGTTCTTGG 1142
	Alignment Scores:	QY	381	AlaLysValGlyLeuTyrAspTyrAspPheGlyLeuGlyLeuGlyAspProGluThrVal 400
	Pred. No.: 2,5e-164 Length: 1336	Db	1143	GCCAAAGTGGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGTAAAGCCGAGACTGTG 1202
	Score: 2296.00 Matches: 444	QY	401	ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420
	Percent Similarity: 100.00% Conservative: 0	Db	1203	AGACGCCCAATCTTTGAGCGCTGTTGAGAGCTTGATGTACTTTATGCCCAAGAGCTGTAT 1262
	Best Local Similarity: 100.00% Mismatches: 0	QY	421	GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440
	Query Match: 98.37% Indels: 0	Db	1263	GGCGAGTTCTGTGCGCGCTTCTCTGAGGGATGAGGATATGACCGGATTTGAAGCGGAT 1322
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		Db	3	ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCAGCTACCGAGGCTCTTTTCGATCTAC 62
		QY	21	ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40
		Db	63	ACCCAAATCAGTCTCTCTACCCCGTCTGATTCCTCTCAATATCCCACTATTGTGACG 122
		QY	41	ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60
		Db	123	ACCTTCGACAGAGTCTTAAGGCTTCTCCGAGCCGCTCCCATGGTCCGACGCCAGGTC 182
		QY	61	LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
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ACCESSION	AF212602	AF212602.1	GI:12003700	QY	101	MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys	120
VERSION	AF212602.1	GI:12003700		DB	303	ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGGCCAAGAAAG	362
KEYWORDS							
SOURCE	Gibberella zeae						
ORGANISM	Gibberella zeae			QY	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
REFERENCE	1 (bases 1 to 1336)			DB	363	AGTTACCTATTGGACCTGGTACCTGGTCCGACGACCCCAAGCGCTGAATTCATTATTCAG	422
AUTHORS	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.			QY	141	LeuAsnPhelIleGlyGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMetAsp	160
TITLE	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab			DB	423	CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAAGCGACGACGCTGTATGGAT	482
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)			QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe	180
MEDLINE	20345085			DB	483	ATGGTAGGCCAAGATGCGGTGATCCGTTCCTCCAGCGCGTCCGTACGACCCCATTC	542
PUBMED	10869425			QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu	200
REFERENCE	2 (bases 1 to 1336)			DB	543	ACCGAAGAGGAATGACGGCCATGACCTCGATCGCAGACGATAGTTCCTTACCTTGAA	602
AUTHORS	O'Donnell, K.			QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly	220
TITLE	Direct Submission			DB	603	AACTATACGATTGGCCCGGAGGTAGATCATCATGTTGTCAAACTCATGTAGTGTGGT	662
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA			QY	221	AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla	240
FEATURES	Location/Qualifiers			DB	663	GACGCTGTTCTCACGCCGTCAGTGCAGCTGGCGCTTCTTCACATTCAGCCCCAGGCC	722
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	KAGYPMAMEDNIIAPKTLIPGPGTDPDPKPVILLQNLFIKGGILVFNQHGAMD			DB	1083	TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTACCAAGCGTCTGCTGAGTCTTGG	1142
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	RGDALVTPVSAWAFPFKPMWSKELDAATKTLDASTKFDVSTDDALSAPFIWKSARV			DB	1143	GCCAAAGTGGGACTCTGGGATTCAGACTTGGGCTCGGACTGGGTAAAGCCGAGCTGTG	1202
	RLEIDGSAFTFCVADVPAMGVSNNTYVGLQNNVTHNSTGTEIANESLGTASRL			QY	401	ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp	420
	RESLDPASMRQTRGLATVLYHNPDKSNVSLTADADPSTVMLSSWAKVGLWDYDGL			DB	1203	AGACGCCCAATCTTTTTCAGGCTGTGTAGAGCTTGTATCTTTATGCCCAAGAGCCCTGAT	1262
	GLGKPEVTRRPFEPVESLMYFMPKPKDGEFCALSLRDEMDRLKADKEWT"			QY	421	GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp	440
ORIGIN				DB	1263	GGCGAGTTCTGTGCGCGCTTCTCTGAGGATGAGATATGACCGATTTGAAGCGCGAT	1322
Alignment Scores:				QY	441	LysGluTrpThr	444
Pred. No.:	5,96e-164	Length:	1336	DB	1323	AAGGAGTGGACC	1334
Score:	2291.00	Matches:	443				
Percent Similarity:	99.77%	Conservative:	0				
Best Local Similarity:	99.77%	Mismatches:	1				
Query Match:	98.16%	Indels:	0				
DB:	8	Gaps:	0				
US-10-614-954-6 (1-451) x AF212602 (1-1336)							
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DB	3	ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCGAGCTCTTCGATCTAC	62				
QY	21	ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer	40				
DB	63	ACCAAAATCAGTCTCTTACCCCGCTCTGATTCCTCTCAATATCCCACTATTGTGACG	122				
QY	41	ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal	60				
DB	123	ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCGCTCCATGGGTGCGAGGCCAGGTC	182				
QY	61	LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp	80				
DB	183	AAAGCCGAGGCGATTACGAGGGGAAACACAGGAACCTCTCTTATCGCTTCCTTTGAGGAC	242				
QY	81	ValProArgValValValLysAspLeuAtcAspAspProSerAlaProThrIleGluGly	100				
DB	243	GTTCTCTCGTGTGTAGTGAAGAACCTCCCGGATGATCTTCAGCACCCAGCATCGAGGGT	302				

RESULT 11

AF212603	AF212603	1336 bp	DNA	linear	PLN 26-JUN-2001
LOCUS	Gibberella zeae strain NRRL6394	trichothecene			
DEFINITION	3-O-acetyltransferase, partial cds.				
ACCESSION	AF212603				
VERSION	AF212603.1	GI:12003702			
KEYWORDS					
SOURCE	Gibberella zeae				
ORGANISM	Gibberella zeae				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.				
AUTHORS	1 (bases 1 to 1336)				
TITLE	O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.				
	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)				
MEDLINE	20345085				
PUBMED	10869425				
REFERENCE	2 (bases 1 to 1336)				
AUTHORS	O'Donnell, K.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA				
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ACCESSION AF212604
VERSION   AF212604.1
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SOURCE    Gibberella zeae
ORGANISM  Gibberella zeae
REFERENCE 1 (bases 1 to 1336)
AUTHORS   O'Donnell, K., Kistler, H.C., Tacke, B.K. and Caspar, H.H.
TITLE      Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE   20345085
PUBMED    10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS   O'Donnell, K.
TITLE      Direct Submision
JOURNAL   Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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 ORGANISM Gibberella zeae

REFERENCE 1 (bases 1 to 1336)  
 AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.  
 TITLE Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)  
 MEDLINE 20345085  
 PUBMED 10869425  
 REFERENCE 2 (bases 1 to 1336)  
 AUTHORS O'Donnell, K.

DIRECT SUBMISSION  
 TITLE Submitted (08-DEC-1999) Microbial Properties Research,  
 JOURNAL NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA  
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AY452807
VERSION
AY452807.1 GI:48527666
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REFERENCE
1. (bases 1 to 1329)
O'Donnell, K., Ward, T.J., Geiser, D.M., Corby Kistler, H. and Aoki, T.
Genealogical concordance between the mating type locus and seven
other nuclear genes supports formal recognition of nine
phylogenetically distinct species within the Fusarium graminearum
clade
Fungal Genet. Biol. 41 (6), 600-623 (2004)
JOURNAL
PUBMED 15121083
REFERENCE
2 (bases 1 to 1329)
O'Donnell, K.
Direct Submission
Submitted (29-OCT-2003) Microbial Genomics, USDA, ARS, 1815 N.
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Query Match: 97.99% Indels: 0
DB: 8 Gaps: 0

US-10-614-954-6 (1-451) x AY452807 (1-1329)

Qy      3  PheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThrGln 22
Db      2  TTCAAGATACAGCTGACACCCCTGGCCAGCTACACAGGCTCTCTTTTCGATCTACACCCAA 61

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Qy      23  IleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThrPhe 42
Db      62  ATCAGTCTCTCTCTACCCCGCTCTCTGATTCTCTCAATATCCCACTATTGTGACACCTTC 121
Qy      43  GluGlnGlyLeuLysArgPheSerGluAlaValProTrrValAlaGlyGlnValLysAla 62
Db      122  GAGCAAGGCTTTAAGCGCTTCTCCGAAGCGTCCCATGGGTGCGACGCCAGGTCAGAGCC 181
Qy      63  GluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValPro 82
Db      182  GAGGCGATTAGCGGGGAAACACAGGAACTTCTTTATCGTCCCTTTTCAGGAGCTTCCT 241
Qy      83  ArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMetArg 102
Db      242  CGTGTGTAGTGAAGACCTCGCGCATGATCTCTCAGCGCCCAACGATCGAGGATATGAGA 301
Qy      103  LysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu 122
Db      302  AAGCGGGGATACCTTATGGCGATGTTTGACGAGAAACATCATCGGCCAAGGAGACGTTA 361
Qy      123  ProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeuAsn 142
Db      362  CTTATTTGACCTGTGTACTGTCCCGACGACCCCAAGGCTGTATTTCTATTGAGCTCAAC 421
Qy      143  PheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetVal 182
Db      422  TTTCATCAAGGGCGGACTCATCTCTACTGTCAACGGACAGCACGCTGCTATGATATGTA 481
Qy      163  GlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGlu 182
Db      482  GGCCAAAGATGCGGTGATCGCTCTACTCTCAAGGCGTCCGTAACACCATTCACCGAA 541
Qy      183  GluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTrrLeuGluAsnTyr 202
Db      542  GAGGAATGACCGCATGAACTCGATCGCAGACGATAGTTCCTTACCTTGAATACTAT 601
Qy      203  ThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAla 222
Db      602  ACGATTGGCCCGCGAGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGTGTCGCT 661
Qy      223  ValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMetSer 242
Db      662  GTTCTCACCGCGTCAGTCAAGCTGGCGGTCTTTCACATTACGCCCAAGGCCATGTCA 721
Qy      243  GluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAsp 262
Db      722  GAGCTCAAGGATGCTGTACCAAGACTCTTGACGCAATCAACAAAGTTCGTGTCGACTGAC 781
Qy      263  AspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAsp 282
Db      782  GATGCTCTTTTCGGCGTTTCATCTGGAATCGGCTCTCGCGTGGCTCTCGAAAGAATCGAT 841
Qy      283  GlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyValSer 302
Db      842  GGCTCTGACCTACCGAGTCTCGCGTGTGTGTGATGTCGACCGCGCAATGGGTGTCTCG 901
Qy      303  AsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIle 322
Db      902  AACAACTACCGAGGCTTCTTCAAAACATGACTTACCACCACTCGACCATCGCGGAATC 961
Qy      323  AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSer 342
Db      962  GCCAAGAGTACTCGGGCAACAGCATCACGCTTTCGTTTCAGAACTCGACCCCGCGAGC 1021
Qy      343  MetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsn 362
Db      1022  ATGCGCCAGCGAACAGAGGCTCTCGCGACGTACTGCAACAACACCCCAAGTCAAC 1081
Qy      363  ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys 382
Db      1082  GTATCCCTGACGGCTGATCGGACCCCATCTACAGCGTCTATGCTGAGTTCCTTGGGCGAAG 1141

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QY	363	ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys	382
Db	1082	GTATCCCTGACGGCTGATCGGACCCATCTACCCAGGTCATGCTGAGTTCTTGGGCCAAG	1141
QY	383	ValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyProGluThrValArgArg	402
Db	1142	GTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGTAAGCCCGAGACTGTGAGACCG	1201
QY	403	ProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGlu	422
Db	1202	CCAATCTTTGAGCCTTTGAGAGCTTGATGTACTTTATGCCCPAGAGCTGTGTGGCGAG	1261
QY	423	PheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGlu	442
Db	1262	TTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGGGATAGGAG	1321
QY	443	TrpThr	444
Db	1322	TGGACC	1327

Search completed: January 24, 2005, 07:55:16  
Job time : 6092 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 23, 2005, 20:29:16 ; Search time 676 Seconds  
(without alignments)  
3502.202 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAFKIQDFTLGLPGLLSY.....EDMDRLKADKEWTKYAYVG 451

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	1356	3	AA54209 Sequence
2	2334	100.0	1356	12	Adn37285 Trichothene
3	2314	99.1	1605	3	Aaz89368 F. gramin
4	1860.5	79.7	1403	3	AA54206 Sequence
5	1860.5	79.7	12949	3	AA54213 Transform
6	1860.5	79.7	13737	3	AA54212 Transform

7	962.5	41.2	1425	3	AA54210 Sequence
8	445.5	19.1	695	3	AAF12071 Aspergill
9	356.5	15.3	1440	10	AD81194 Orfil cod
10	356.5	15.3	72149	10	AD81173 ML-236B s
11	351	15.0	482	8	AB254817 Aspergill
12	175	7.5	1508	12	AD070366 Barley ag
13	170.5	7.3	1587	10	ABX78350 Wheat str
14	170.5	7.3	1596	3	AAC38228 Arabidops
15	169.5	7.2	1593	3	AAC49441 Arabidops
16	168.5	7.2	1735	10	ABX78344 Corn stre
17	166.5	7.1	1455	8	ADA70751 Rice gene
18	165.5	7.1	1207	12	AD070371 Barley ag
19	161	6.9	1556	10	ABX78348 Soybean s
20	158.5	6.8	1241	12	AD070384 Barley ag
21	157.5	6.7	1220	12	AD070368 Wheat par
22	154.5	6.6	1296	3	AAC64783 Mango alc
23	154	6.6	1471	3	AAC40295 Arabidops
24	151.5	6.5	1605	2	AAT37310 Aromatic
25	143	6.1	1428	6	AB213585 Arabidops
26	143	6.1	1428	6	ADG88181 A. thalia
27	143	6.1	1428	6	ADG87834 A. thalia
28	143	6.1	1428	8	ADA68064 Arabidops
29	143	6.1	1428	12	ADN72452 Thale cre
30	143	6.1	1551	3	AAC48784 Arabidops
31	142.5	6.1	1329	3	AAC45418 Arabidops
32	142.5	6.1	1471	3	AAC45423 Arabidops
33	142	6.1	1347	5	AAD03360 Taxus cus
34	142	6.1	1347	10	ADB91966 Acyltrane
35	141.5	6.1	1452	8	ADA69994 Rice gene
36	139.5	6.0	1815	3	AAC48422 Arabidops
37	139.5	6.0	3499	6	AAD41127 Arabidops
38	139.5	6.0	7438	6	AAD41126 Arabidops
39	135	5.8	1542	2	AAQ54685 Anther sp
40	134.5	5.8	1477	3	AAC39128 Arabidops
41	134	5.7	3706	2	AAQ54693 Anther sp
42	134	5.7	3706	2	AAQ58340 Tobacco A
43	132.5	5.7	1125	3	AAC40902 Arabidops
44	132.5	5.7	83698	6	ABN85767 Arabidops
45	132	5.7	1317	5	AAD03346 Taxus cus

ALIGNMENTS

RESULT 1  
AAA54209 standard; DNA; 1356 BP.  
XX AAA54209;  
AC AAA54209;  
XX  
DT 15-SEP-2003 (revised)  
DT 26-FEB-2001 (first entry)

Sequence encoding trichothecene resistance polypeptide.

Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;  
wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
ds.

Gibberella zeae.

Key Location/Qualifiers  
CDS 1..1356  
FT /tag= a  
FT /product= "Trichothecene resistance polypeptide"

XX WO200060061-A2.

PD 12-OCT-2000.

XX 29-MAR-2000; 2000WO-EP002769.

XX 31-MAR-1999; 99US-00282995.

PR 11-FEB-2000; 2000US-00502852.

XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX  
XX Hohn TM, Peters C, Salmerson JM, Reed JN, Dawson JL;  
DR WPI; 2000-679374/66.  
DR P-PSDB; AAB03935.  
XX  
XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
PT or rice plant, comprises heterologous polynucleotide encoding gene  
PT product expressed in cell, having trichothecene resistance activity.  
XX  
XX Claim 8; Page 48-49; 62pp; English.  
PS  
XX A heterologous gene encoding a gene product which confers trichothecene  
CC resistance can be used to transform plant cells to make them resistant to  
CC fungal infection. The transformation method is useful for preventing  
CC mycotoxin contamination of a plant, particularly a crop plant such as  
CC wheat, maize, barley or rice, and for reducing and/or preventing the  
CC growth of a fungus of the genus Fusarium that produces a trichothecene,  
CC preferably comprising a C-3 hydroxyl group, by growing transformed crop  
CC plants in an area which is moderate to severe fungal infestation.  
XX (Updated on 15-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3-7e-219 Length: 1356  
Score: 2334.00 Matches: 451  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-614-954-6 (1-451) x AAAS4209 (1-1356)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20  
DB 1 ATGGCTTTCAAGATACAGTCCGACACCTCGGCGAGTACCAAGCCCTCTTCGATCTAC 60  
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerClnTyrProThrIleValSer 40  
DB 61 ACCCAATCAGTCTCTCTACCCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120  
QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60  
DB 121 ACCTTCGACAGGCTTTAAGCGCTTCTCGAAGCGTCCCATGGGTCCGAGGCCAGGTC 180  
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
DB 181 AAAGCCGAGGGCAATTAGCGAGGGAACACAGGAACCTTCCTTTATCGTCCCTTTGAGGAC 240  
QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100  
DB 241 GTTCTCTGGTGTGTAGTGAAGACCTCCCGGATGATCCTTCAGCGCCACGATCGAGGT 300  
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys 120  
DB 301 ATGAGAAAGCGGGATACCTATGGCGATGTTGACGAGAACATCATCGGCCAAGGAAG 360  
QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln 140  
DB 361 ACGTTACCTATTGGACCTGCTACTGGTCCGACGACCCAAAGCCTGTATTCTATTGACG 420  
QY 141 LeuAsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
DB 421 CTCACCTTCATCAAGGGCGGATCATCTCTACGTCAACGGACGACCGTCTATGGAT 480  
QY 161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180  
DB 481 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAGGCGTGGCGTAACGCCCATTC 540

QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200  
DB 541 ACCGAGAGGAAATGACGGCCATGAACTCGATCGCAACGATAGTTCTTACCTTGA 600  
QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220  
DB 601 AACTATACGATTGGCCCGGAGGTAGATCATCATGTTGTCAAAGCTGATAGTGTGGT 660  
QY 221 AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla 240  
DB 661 GACGCTGTCTCAGCGCGGTGAGTGCAGCTGGCGTCTTTCACATTCAGCCCCAAGGCC 720  
QY 241 MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260  
DB 721 ATGTCAAGAGCTCAAGGATGCTCTACCAAGACTCTTGACGCATCAACAAGTTCTGTGTCG 780  
QY 261 ThrAspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArg 280  
DB 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAATCGGCTCTCGGTGGTCTCGAAAGA 840  
QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
DB 841 ATCGATGGCTCTGACCTACCGAGTCTGCGGTCTGTGTGATGCTCGACCGCAATGGT 900  
QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320  
DB 901 GTCTCGAACAACTACCCAGGCTTCTTCAAAACATGACCTACCACTCGACCATCGGC 960  
QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340  
DB 961 GAAATCGCCCAACGAGTCACTCGGCGCAACAGCATCACGCTTCGTTCAGAACTCGACCCC 1020  
QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360  
DB 1021 GCGAGCATGGCGCAGGACACAGAGGTCTCGCGAGCTACTGTCACACACCCCGACAG 1080  
QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp 380  
DB 1081 TCCAAAGTATCTCTGACGCTGATCGGACCCATCTACGAGGTCATGCTGAGTCTTTGG 1140  
QY 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400  
DB 1141 GCCAAGGTGGGACTCTGGGATTAACGACTTGGGCTCGGAGTGGGTAAAGCCGAGACTGTG 1200  
QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420  
DB 1201 AGACGCGCAATCTTTGAGCGCTTTCAGAGCTTGATGTACTTTATGCCCAAGAGCTGAT 1260  
QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440  
DB 1261 GCGGAGTTCGTGCGCGCTTCTCTGAGGGATGAGGATATGACCGGATTTGAAGCGGAT 1320  
QY 441 LysGluTyrTrpLysTyrAlaGlnTyrValGly 451  
DB 1321 AAGGAGTGACCAAGTATGCGGAGTACGTGTGT 1353

RESULT 2  
ADN37285  
ID ADN37285 standard; DNA; 1356 BP.  
XX  
AC ADN37285;  
XX  
DT 15-JUL-2004 (first entry)  
DE Trichothecene 3-O-acetyltransferase encoding DNA SEQ ID NO:29.  
XX  
XX maternal tissue; plant seed; plant;  
KW bifunctional alpha-amylase subtilisin inhibitor gene promoter;  
KW alpha-amylase inhibitor promoter; ASI promoter; plant protectant;  
KW virucide; vaccine; resistance; infection; Fusarium graminearum;  
XX trichothecene 3-O-acetyltransferase; enzyme; gene; ds.  
OS Gibberella zeae.

XX	Key	Location/Qualifiers	QY	1	MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr	20
FH	CDS	1..1356	Db	1	ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAAGGCTCTCTTTCATCTAC	60
FT		/tag= a				
FT		/product= "Trichothecene 3-O-acetyltransferase protein"				
XX	WO2004035790-A1.		QY	21	ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer	40
XX	29-APR-2004.		Db	61	ACCAAAATCAGTCTCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTGTGACG	120
XX	17-OCT-2003; 2003WO-AU001381.		QY	41	ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal	60
XX	17-OCT-2002; 2002AU-00952143.		Db	121	ACCTTCGAGCAAGGCTTAAGCGCTTCTCCGAAGCGCTCCCATGGGTGCGCAGCCAGGTC	180
XX	(MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.		QY	61	LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp	80
PA	(GRAI-) GRAINS RES & DEV CORP.		Db	181	AAAGCCGAGGGCATTTAGCGAGGGAACACAGGAACCTCTCTTATCGTCCCTTTTGAAGAC	240
XX	Furtado A, Henry RJ;		QY	81	ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly	100
XX	WPI; 2004-348462/32.		Db	241	GTTCCTCGGTGTGTAGTGAAGACCTCCGCGATGATCTTCAGCGCCCAAGATCGAGGTT	300
XX	P-PSDB; ADN37286.		QY	101	MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLys	120
PT	Expressing nucleic acid or protein in a plant seed, useful in enhancing		Db	301	ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAG	360
PT	resistance of a plant against Fusarium graminearum and barley stripe		QY	121	ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln	140
PT	mosaic virus, comprises expressing a bifunctional alpha-amylase		Db	361	ACGTTACCTATTGGACCTGGTACTGGTCCGACGACCCCAAGCCTGTAATCTTATTGCGAG	420
PT	subtilisin inhibitor promoter.		QY	141	LeuAsnPheIleGlyGlyLeuIleThrValAsnGlyGlnHisGlyAlaMetAsp	160
PS	Claim 20; SEQ ID NO 29; 169pp; English.		Db	421	CTCAACTTCATCAAGGGCGGACTCATCTCTCAAGCGTCCGTCGATGCGTATGGAT	480
XX	The present invention describes a method for expressing nucleic acid or		QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe	180
XX	protein in the maternal tissue of a plant seed. The method comprises		Db	481	ATGGTAGGCCAAGATGGGTGATCCGTCTCTCAAGCGTCCGTCGATGCGTATGGAT	540
XX	expressing isolated nucleic acid operably under the control of a		QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProThrLeuGlu	200
XX	bifunctional alpha-amylase subtilisin inhibitor (ASI) gene promoter that		Db	541	ACCGAAGAGGAAATGACGGCCATGAACCTCGATCGCAGACGATAGTCTTACCTTGAA	600
XX	is operable in the maternal tissue. Also described: (1) a method of		QY	201	AsnThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly	220
XX	enhancing or conferring resistance of a plant against: (a) Fusarium		Db	601	AACTATACGATTGGCCCCGAGGTAGATCATCATGATGTCAGATTGTCAAAGCTGATGAGTGGT	660
XX	graminearum (head scab); and (b) barley stripe mosaic virus (BSMV); (2)		QY	221	AspAlaValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAla	240
XX	an isolated transformed wheat and barley seed that expresses isolated		Db	661	GAAGCTGTTCTCAGCGCGGTGAGTGCAGCTGGCGTCTTTCACATTCAGCCCAAGGCC	720
XX	nucleic acid encoding respectively a plant defence protein and a BSMV		QY	241	MetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSer	260
XX	coat protein or an inhibitory RNA that prevents, inhibits or reduces		Db	721	ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTTGACGCATCAACAAGTTCTGTGTCG	780
XX	expression of a BSMV movement protein placed operably under the control		QY	261	ThrAspAlaLeuSerAlaPheIleThrLysSerAlaSerArgValArgLeuGluArg	280
XX	of the ASI gene promoter where the seed exhibits enhanced resistance		Db	781	ACTGACGATGCTCTTTCGGCGTTCATCTGGAATCGGCCCTCTCGCGTGGTCTCGAAGA	840
XX	against Fusarium graminearum (head scab) and BSMV by virtue of the		QY	281	IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly	300
XX	presence of the nucleic acid compared to an otherwise isogenic line that		Db	841	ATCGATGGCTCTGCACCTACCGAGTTCGCCGTGCTGTGTGATGCTCGACCGCAATGGGT	900
XX	does not express the nucleic acid placed operably under the control of		QY	301	ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly	320
XX	the ASI gene promoter; (3) a method of producing an immunogenic		Db	901	GTCTCGAACCAACTACCCAGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC	960
XX	tissue of a plant seed produced by a process that comprises performing		QY	321	GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro	340
XX	the method of (1); (5) a method of enhancing the nutritional quality of		Db	961	GAATCGCCCAACGAGTCACTCGCGCAACAGCATCAACGCTTCGTTTTCAGAACTCGACCCC	1020
XX	bran or animal fodder; and (6) an isolated bran or maternal tissue of a		QY	341	AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys	360
XX	seed produced by a process that comprises performing the method of (5).		Db	1021	GCAGCATCGCGCAGGAAACAGAGGTCTCGCGAGTACTCTGCACCAACACCCCGACAG	1080
XX	The composition has plant protectant and virucide activities, and can be					
XX	used in vaccines. The method is useful in expressing nucleic acid or					
XX	protein in the maternal tissue of a plant seed. The method and ASI gene					
XX	promoter are useful in enhancing or conferring resistance of a plant					
XX	against Fusarium graminearum and BSMV and in enhancing the nutritional					
XX	quality of bran or animal fodder. The seed or bran product and the					
XX	composition are useful as an oral vaccine against infection in the					
XX	gastrointestinal, respiratory and urogenital tracts. The present sequence					
XX	encodes the Fusarium graminearum (Gibberella zeae) trichothecene 3-O-					
XX	acetyltransferase, which is used in the exemplification of the present					
XX	invention.					
SQ	Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 U; 0 Other;					

## Alignment Scores:

Pred. No.:	3,7e-219	Length:	1356
Score:	2334.00	Matches:	451
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-614-954-6 (1-451) x ADN37285 (1-1356)

QY 361 SerAsnValSerLeuThrAlaAspProSerThrSerValMetLeuSerSerTyr 380  
 Db 1081 TCCAAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAAGCGTCATGCTGAGTTCTGG 1140  
 QY 381 AlalyseValGlyLeuTyrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400  
 Db 1141 GCCAAGTGGGACTCTCGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTG 1200  
 QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420  
 Db 1201 AGACGCCCATCTTTGAGCCCTGTTGAGAGCTTGATGTACTTTATGCCAAGAGCTGTAT 1260  
 QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440  
 Db 1261 GGGGAGTTCTGTGGCGGCTTTCTCTGAGGGATGAGGATATGACCCGATTGAAGGGCGGAT 1320  
 QY 441 LysGluTyrThrLysTyrAlaGlnTyrValGly 451  
 Db 1321 AAGGATGGACCAAGTATGCGCAGTACGTTGGT 1353

## RESULT 3

AAZ89368  
 ID AAZ89368 standard; DNA; 1605 BP.

AC AAZ89368;  
 XX  
 DT 15-SEP-2003 (revised)  
 DT 09-JUN-2000 (first entry)  
 XX  
 DE F. graminearum trichothecene 3-O-acetyltransferase DNA.  
 XX  
 KW Trichothecene 3-O-acetyltransferase; selective marker; ds.  
 XX  
 OS Gibberella zeae.

FH Key Location/Qualifiers  
 FT CDS 135..1490  
 FT /\*tag= a  
 FT /product= "trichothecin 3-O-acetyltransferase"

XX JP2000032985-A.

XX 02-FEB-2000.

PF 15-JUL-1998; 98JP-00200280.

PR 15-JUL-1998; 98JP-00200280.

PA (RIKA ) RIKAGAKU KENKUSHO.

PA (YAMA/) YAMAGUCHI I.

XX WPI; 2000-274037/24.

DR P-PSDB; AAY51848.

XX Trichothecin 3-O-acetyltransferase gene useful as a selective marker in  
 PT gene manipulations in eukaryotic host cells.

PS Claim 3; Page 16-18; 25pp; Japanese.

CC This invention describes a novel protein with trichothecin 3-O-  
 CC acetyltransferase activity. The gene is used as a selective marker in a  
 CC gene manipulation using eukaryote as the host cell. This sequence encodes  
 CC the trichothecin 3-O-acetyltransferase isolated from *Fusarium*  
 CC *graminearum*. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 1605 BP; 397 A; 459 C; 393 G; 356 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4,32e-217 Length: 1605  
 Score: 2314.00 Matches: 447  
 Percent Similarity: 99.11% Conservative: 0  
 Best Local Similarity: 99.11% Mismatches: 4  
 Query Match: 99.14% Indels: 0

Db: 3 Gaps: 0  
 US-10-614-954-6 (1-451) x AAZ89368 (1-1605)  
 QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20  
 Db 135 ATGGCTTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCAAGGCCTCCTTTGATCTAC 194  
 QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40  
 Db 195 ACCCAATCAGTCTCTCTACCCCGTCTCTGATCCCTCTCAATATCCCACTATTGTTCAGC 254  
 QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60  
 Db 255 ACCTTCGACCAAGGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGTTCGACGCCAGGTC 314  
 QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
 Db 315 AAAGCCGAGGGCATTTAGCGAGGGAACACCGGAACCTCTTATCGTCTCTTTTGGAGAC 374  
 QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100  
 Db 375 GTTCTCGTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 434  
 QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120  
 Db 435 ATGAGAAAGGGCGGATACCTTATGGCGATGTTTTCGAGAGAACATCATCGCGCCAGGAAG 494  
 QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGln 140  
 Db 495 ACCTTACCTATTGGACCTGTGTACTGGCCCGACGACCCCAAGCCTGTGATTTATTCGAC 554  
 QY 141 LeuAsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
 Db 555 CTCAACTTCATCAGGGCGGACTCATCTCACTGTCACGAGACAGACGGTCTTATGGAT 614  
 QY 161 MetValGlyGlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPhe 180  
 Db 615 ATGGTAGGCCAAGATGCGGTGATCGCTCTACTCTCCAAAGCGTCCGTAACGACCATTC 674  
 QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200  
 Db 675 ACCGAAGAGGAATGACGGCCCATGAACCTCGATCCGAAGACGATAGTTCCTTACCTTGAA 734  
 QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220  
 Db 735 AACTACAGATTGGCCCGAGGTAGATCATCAGATTGTCAAACCTGATGTAGTGTGGT 794  
 QY 221 AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla 240  
 Db 795 GACGCTGTTCTCACGCCGCTCAGTCAAGCTGGGCGTCTTCAAAATTCAGCCCAAGGCC 854  
 QY 241 MetSerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260  
 Db 855 ATGTCAAGAGCTCAAGGATGCTGTACCAAGACTCTTTCAGCGCATCAACAAAGTTCGTGCG 914  
 QY 261 ThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280  
 Db 915 ACTGACGATGCTCTTTCCGGCTTCATCTGGAATCCGGCTCTCCGGTGGCTCCGAAGA 974  
 QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
 Db 975 ATCGATGGCTCTGCAACCTTACCGAGTCTTCGCGGTGCTGTGTGATGCTCGACCGCAATGGGT 1034  
 QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320  
 Db 1035 GTCTGAAACAATCCCAAGGCTTCTTCAAAACATGACCTACCAACTCCGACCATCGCC 1094  
 QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGlyLeuAspPro 340  
 Db 1095 GAAATCGCAACGAGTCTACTCGCGCAACAGCATCAGCCCTTCGTTTCAAGATCGTACGCC 1154  
 QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360



Db 1155 GCAGATGCGCCAGGAAACAGAGTCTCGGACGTACCTGCACAAACCCCGCAAG 1214  
 QY 361 SerAsnValSerLeuThrAlaAepAlaAepProSerThrSerValMetLeuSerSerTrp 380  
 Db 1215 TCCAAAGTATCTCTGACGGCTGATGCGGACCCATCTACCAAGCTCATGCTGAGTCTTGG 1274  
 QY 381 AlaLysValGlyLeuTrpAspThrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400  
 Db 1275 GCCAAGTCCGACTCTGGGATTACGACTTTGGTTCGGACTGGGTAAGCCGAGACTGTG 1334  
 QY 401 ArgArgProIlePheGluProValGluSerLeuMetThrPheMetProLysLysProAsp 420  
 Db 1335 AGACGCCCAATCTTTGAGCGCTGTGAGAGCTGTGATCTTTATGCCCCAAGAGCCTGAT 1394  
 QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440  
 Db 1395 GCGAGTCTGTGCGGGCTTTCTCTGAGGATGAGGATGATGACCGATTGAAGGGCGAT 1454  
 QY 441 LysGluTrpThrLysThrAlaGlnThrValGly 451  
 Db 1455 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGT 1487

## RESULT 4

AAA54206

ID AAA54206 standard; cDNA; 1403 BP.

XX

AC AAA54206;

XX

DT 26-FEB-2001 (first entry)

XX

DE Sequence encoding trichothecene resistance polypeptide.

XX

KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;  
 wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
 ds.

XX

OS Fusarium sporotrichioides.

XX

FH Key Location/Qualifiers

FT 7..1386

FT CDS

FT /\*tag= a

FT /product= "Trichothecene resistance polypeptide"

XX

XX W0200060061-A2.

XX

PD 12-OCT-2000.

XX

XX 29-MAR-2000; 2000WO-EP002769.

XX

XX 31-MAR-1999; 99US-00282995.

XX

XX 11-FEB-2000; 2000US-00502852.

XX

XX (NOVS ) NOVARTIS AG.

XX

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX

XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

XX

XX WPI: 2000-679374/66.

XX

XX P-PSDB; AAB03934.

XX

PT Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
 or rice plant, comprises heterologous polynucleotide encoding gene  
 product expressed in cell, having trichothecene resistance activity.

XX

XX Claim 8; Page 46; 62pp; English..

XX

CC A heterologous gene encoding a gene product which confers trichothecene  
 resistance can be used to transform plant cells to make them resistant to  
 fungal infection. The transformation method is useful for preventing  
 mycotoxin contamination of a plant, particularly a crop plant such as  
 wheat, maize, barley or rice, and for reducing and/or preventing the  
 growth of a fungus of the genus Fusarium that produces a trichothecene,

CC

CC

CC

CC

CC

CC preferably comprising a C-3 hydroxyl group, by growing transformed crop  
 plants in an area which is moderate to severe fungal infestation

XX

SQ Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.23e-172 Length: 1403  
 Score: 1860.50 Matches: 349  
 Percent Similarity: 88.67% Conservative: 50  
 Best Local Similarity: 77.56% Mismatches: 50  
 Query Match: 79.71% Indels: 1  
 DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x AAA54206 (1-1403)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThr 21

Db 37 TCTTTGACATAGAGCTCGACATCATCGCCGAGCAACCCGCTCTTCTTCAATCTACACC 96

QY 22 GlnIleSerLeuLeuThrProValSerAspSerSerGlnThrProThrIleValSerThr 41

Db 97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 156

QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61

Db 157 CTTGAGGAAGGCTTAAACGCTCTCTCAACCTTCCCATGGTCCGGCCAGGTCAG 216

QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81

Db 217 ACCGAGGCGATCAGCGAGGAAACACAGGAACCTTCCAAGATCATTCATGAGGAGACA 276

QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101

Db 277 CCCCCTCTTGTGTGAAAGACCTCCGTGATGATTCCTCAGCGCAACGATCGAGGGGTG 336

QY 102 ArgLysAlaGlyThrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121

Db 337 AGAAAGCGGGTTCCTCCCTTAGAGATGTTTACGAGAACGTCGCTCCGAGGAAGACA 396

QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141

Db 397 TTAGCTATCGGACCTGGCAATGCCCCCAACGACCGGAGCCTGTGTCTATTGACAGTC 456

QY 142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161

Db 457 AACTTCATTAAAGCGGACTCATTTCTACCGTCAACGCAACATGGTGTATGGACATG 516

QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181

Db 517 ACAGGACAAAGATGCAATTATTCGTCTCTCAAGCGTCCGCAACGAATCATTCACC 576

QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProThrLeuGluAsn 201

Db 577 GAGGAGAAATCTCGGCCATGAACCTCGATCGCAGACGGTAGTCTCTCTTGAANAAC 636

QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyLys 221

Db 637 TACAAAGTTGGTCTCGAGCTAGACCAACACAGATCGCCAAACCTCGCGCTGCT---GGCGAC 693

QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241

Db 694 GTCCACCCCGCCCGCCCAAGCGAGTCTTTTCAATTCATCTCCCAAGGGCCCTC 753

QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261

Db 754 TCGAGCTGAAAGACGACGACCAAGACTCTTGAGCGCTCGTCCAGTTTGTGTCACT 813

QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281

Db 814 GATGATGCTCTTTGCGCGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 873

QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301

Db 874 GATGCTTCCACACTACTGAATTCCTGCCGCGCTGTGACATGCGGGGCCCAATATGGCGGTA 933

Qy 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321

Db 934 TCAGACATACCCAGCGCTTCTTCAAAACATGACCTACCATGACCTGCGACCTGCGCGAA 993

Qy 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuLeuAspProAla 341

Db 994 ATGCCCAACGACACTTGGCGCAACAGCATCACGCTGCGCTCGGAACCTCAACAGTGAT 1053

Qy 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361

Db 1054 CGTTTGGCAGACGAAACACAAAGCTTTGGCGACGTATCATGCTGCGCTGCAAGTCG 1113

Qy 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381

Db 1114 AGCGTCTCCTGACCGCGGATGCGAATCCGTCAGCAGCATCATGTGAGTCTCTGGGCC 1173

Qy 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401

Db 1174 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTGGACTGGGTAAAGCTGAGAGTGTGAGA 1233

Qy 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421

Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGATCTTTATGCCCAAGAGCCTGATGG 1293

Qy 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441

Db 1294 GAGTTTACGGCGTCCATTTCTCGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 1353

Qy 442 GluTrpThrLysTyrAlaGlnTyrValGly 451

Db 1354 GAGTGACAAAGTACGCAAGTATATTGGG 1383

RESULT 5

ID AAA54213 standard; DNA; 12949 BP.

AC AAA54213;

XX 26-FEB-2001 (first entry)

XX Transformation vector pNOV1704.

DE Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;

KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;

KW ds.

XX Synthetic.

OS W0200060061-A2.

XX 12-OCT-2000.

XX 29-MAR-2000; 2000MO-BP002769.

PF 31-MAR-1999; 99US-00282995.

XX 11-FEB-2000; 2000US-00502852.

PR (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

PI WPI; 2000-679374/66.

XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley

PT or rice plant, comprises heterologous polynucleotide encoding gene

PT product expressed in cell, having tricothecene resistance activity.

XX Disclosure; Page 58-62; 62pp; English.

PS A heterologous gene encoding a gene product which confers tricothecene

XX

CC resistance can be used to transform plant cells to make them resistant to

CC fungal infection. The transformation method is useful for preventing

CC mycotoxin contamination of a plant, particularly a crop plant such as

CC wheat, maize, barley or rice, and for reducing and/or preventing the

CC growth of a fungus of the genus Fusarium that produces a tricothecene,

CC preferably comprising a C-3 hydroxyl group, by growing transformed crop

CC plants in an area which is moderate to severe fungal infestation. Plasmid

CC pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose

CC isomerase selectable marker and the nopaline synthase termination

CC sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter

CC operably linked to the tricothecene 3-O-acetyl transferase sequence

CC given in GENESSEQ record AAA54206 and the nos termination sequence

XX

SQ Sequence 12949 BP; 3194 A; 3146 C; 3143 G; 3466 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2,85e-171	Length:	12949
Score:	1860.50	Matches:	349
Percent Similarity:	88.67%	Conservative:	50
Best Local Similarity:	77.56%	Mismatches:	50
Query Match:	79.71%	Indels:	1
DB:	3	Gaps:	1

US-10-614-954-6 (1-451) x AAA54213 (1-12949)

Qy 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21

Db 11282 TCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTTCTTTCATCTACACC 11341

Qy 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41

Db 11342 CAGATCAGTCTCGTTTACCCCGTCTGTATCCCTCCAGTATCCCAACATCGTCAGCACC 11401

Qy 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61

Db 11402 CTTGAGGAGGCGCTAAACGCTCTCTCAACCTTCCCACTGGGTGCGGGCCAGGTCAAG 11461

Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81

Db 11462 ACCGAGGGCATCAGCGAGGAAACACAGAACTTCCAGATCATTCATATGAGGAGACA 11521

Qy 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101

Db 11522 CCCCCTCTGTGTGAAAGACCTCGGTGATGATTCCTCAGCGCCCAACGATCGAGGGGTG 11581

Qy 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121

Db 11582 AGAAAGGCGGGTTTCCCTTAGAGATGTTTGACGAGAACGTCGTCCTCCGAGGAGACA 11641

Qy 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141

Db 11642 TTAGCTATCGGACCTGGCAATGCCCCAACGACCGAGCGCTGTGTGCTATTGAGCTC 11701

Qy 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161

Db 11702 AACTTCATTAGGCGGAGCTCATTCACCGTCAACGAGCAACACATGGTGTCTATGACATG 11761

Qy 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181

Db 11762 ACAGGACAAAGATGCATATTCTCTCTCAAGGCGTCCGCAACGAATCATTCACC 11821

Qy 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProThrLeuGluAsn 201

Db 11822 GAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCCCTCTCTTGAACA 11881

Qy 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221

Db 11882 TACAAAGTTGGTCTCTGAGCTAGACACACAGATCGCAAACTCGCCCTGCT---GCGGAC 11938

Qy 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241

Db 11939 GCTCCACCGGACCGGCCAAGGCAAGCTGGGCGTCTCTTTTCATTCATCCCAAGGCCCTC 11998

QY 242 SerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261  
 DB 11999 TCGAGCTGAAGACGACGACCAAGACTTTGACGCTCGTCCAAAGTTTGTCAACT 12058  
 QY 262 AspAspAlaLeuSerAlaPheLeuTTPlysSerAlaSerArgValArgLeuGluArgIle 281  
 DB 12059 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTAGCTCTCGCAAGATTG 12118  
 QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaSerProAlaMetGlyVal 301  
 DB 12119 GATGCTTCACACCTACTGAATTTCTCCGCGCTGTGCACATGCGGGGCCCAATGGCGTA 12178  
 QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321  
 DB 12179 TCAAGCACATACCCAGCGCTTCTTCAAAACATGACCTACCATGACCTCGCGCGAA 12238  
 QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341  
 DB 12239 ATCGCCACGAACCACTTGGCGACAGCATCAGCGCTCGCTCGGAACTCAACAGTGAT 12298  
 QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361  
 DB 12299 CGTTTCGCGACAGCAACAGCTTTGGCGAGCTACATGATGCGCTGACAAAGTCG 12358  
 QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381  
 DB 12359 AGCGTCTCCCTGACCCCGATCGAATCGTCAAGCAGCATCATGTGATGTTCTTGGGCG 12418  
 QY 382 LysValGlyLeuTTPAspTyrAspPheGlyLeuGlyLeuGlyProGluThrValArg 401  
 DB 12419 AAGTGGGATGCTGGGAGTATGACTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 12478  
 QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421  
 DB 12479 AGACCTCGCTTTGAACCTTTTGAGAGTTTGTGATCTTTATGCCCAAGAGCTGATGG 12538  
 QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441  
 DB 12539 GAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 12598  
 QY 442 GluTTPThrLysTyrAlaGlnTyrValGly 451  
 DB 12599 GAGTGGCAAAAGTACGCAAGTATATTGGG 12628  
 RESULT 6  
 ID AAA54212  
 XX AAA54212 standard; DNA; 13737 BP.  
 AC AAA54212;  
 XX  
 DT 26-FEB-2001 (first entry)  
 XX  
 DE Transformation vector pGROTRIR.  
 XX  
 KW Tricothecene resistance; resistant; crop protection; mycotoxin; fungus;  
 KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
 KW ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200060061-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 29-MAR-2000; 2000WO-EP002769.  
 XX  
 PR 31-MAR-1999; 99US-00282995.  
 PR 11-FEB-2000; 2000US-00502852.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;

XX WPI; 2000-679374/66.  
 XX Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
 PT or rice plant, comprises heterologous polynucleotide encoding gene  
 PT product expressed in cell, having tricothecene resistance activity.  
 XX  
 PS Disclosure; Page 54-58; 62pp; English.  
 XX  
 CC A heterologous gene encoding a gene product which confers tricothecene.  
 CC resistance can be used to transform plant cells to make them resistant to  
 CC fungal infection. The transformation method is useful for preventing  
 CC mycotoxin contamination of a plant, particularly a crop plant such as  
 CC wheat, maize, barley or rice, and for reducing and/or preventing the  
 CC growth of a fungus of the genus Fusarium that produces a tricothecene,  
 CC preferably comprising a C-3 hydroxyl group, by growing transformed crop  
 CC plants in an area which is moderate to severe fungal infestation. Plasmid  
 CC pGROTRIR comprises a selectable marker operably linked to a promoter and  
 CC terminator sequence and the tricothecene resistance gene described in  
 CC GENESSEQ record AAA54206 behind and in frame with the Arabidopsis thaliana  
 CC UBI 3 promoter and in front of and in frame with the nos polyadenylation  
 CC signal  
 XX  
 SQ Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3.1e-171 Length: 13737  
 Score: 1860.50 Matches: 349  
 Percent Similarity: 88.67% Conservative: 50  
 Best Local Similarity: 77.56% Mismatches: 50  
 Query Match: 79.71% Indels: 1  
 DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x AAA54212 (1-13737)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21  
 DB 51 TCTTTTGACATAGCTCGACATCATCGGCCAGCAACCGCCTCTTCTTCAATCTACACC 110  
 QY 22 GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr 41  
 DB 111 CAGATCAGTCTCGTTTACCCCGTCTCTGATCTCCCATGCCACCATCGTCAGCACC 170  
 QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTTPValAlaGlyGlnValLys 61  
 DB 171 CTTGAGGAAGGCTAAACCGCTCTCTCAACCTTCCCATGGTCCGCGGCCAGGTCAG 230  
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81  
 DB 231 ACCGAGGGCATCAGCAAGGAACACAGGAACCTTCCAAGATCATTCATGAGGAGACA 290  
 QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101  
 DB 291 CCCCTCTTGTGTGAAGACCTCGTGATGATCTCTAGCGCCCAACGATCAGGGGGTTG 350  
 QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121  
 DB 351 AGAAAGCGGGTTTCCCTTAGAGATGTTTACGAGAACGTCGTCGCTCCGAGGAAGACA 410  
 QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGlnLeu 141  
 DB 411 TTAGCTATCGGACCTGGCAATGGCCCAACGACCCGCAAGCCTGTGTGTTGATTCGAGCTC 470  
 QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161  
 DB 471 AACTTCATTAAAGGGCGGACTCATTTCCACCGTCAACGGCAACATGGTCTATGACATG 530  
 QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181  
 DB 531 ACAGGACAAGATGCAATTTATGCTCTCTCTCAAGGGCGTCCGCAACGAATCATTCACC 590  
 QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrThrGluAsn 201

Db 591 GAGGAGAAATCTCGGCCATGAACCTCGATCGAAGACGGTAGTCCCTCTCTTGAAGAAC 650  
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221  
Db 651 TACAAAGTTGGTCTGAGCTAGACCACCAAGTGGCGCTCTTTTATCTACTCCCAAGGCCCTC 707  
QY 222 AlavalLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241  
Db 708 GCTCCACCCGACCGGCCAAGCAAGCTGGCGCTCTTTTATCTACTCCCAAGGCCCTC 767  
QY 242 SerGluLeuIysAspAlaAlaThrLysThrLysAlaSerThrLysPheValSerThr 261  
Db 768 TCGGAGCTGAAGACGACGACCAAAAGACTTTGAGCGCTGCTGCAAGTTGTGTCAACT 827  
QY 262 AspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArgIle 281  
Db 828 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 887  
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301  
Db 888 GATGCTTCCACACCTACTGAATCTGCGCGCTGTGACATGCGGGGCCCAATGGGCGTA 947  
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321  
Db 948 TCAAGCACATATCCAGCGCTTCTCAAAACATGACCTACATGACCTCGACCGCTCGCGAA 1007  
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341  
Db 1008 ATGCGCCACGACCACTTGGCGCAACAGATCAAGCTGGCTGGCAATCAACAGTGAT 1067  
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361  
Db 1068 CGTTTGGCAGACGACACAAAGCTTTGGCGACGTACATGACCTGCGCTGCAAGTCG 1127  
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381  
Db 1128 AGCGTCTCCCTGACCGCCGATCGAATCGTCAAGCAGCATGCTGAGTTCTCTGGGCC 1187  
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThrValArg 401  
Db 1188 AAGTGGGATCTGGGAGTATGACTTGGTTGGATCTGGTAAGCTGAGAGTGTGAGA 1247  
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421  
Db 1248 AGACCTCGCTTGAACCTTTGAGAGCTTTCATGATCTTTATGCCCCAAGAGCTGATGG 1307  
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441  
Db 1308 GAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGGAGAGACTAAAGGCGGATGAG 1367  
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451  
Db 1368 GAGTGACAAAGTACGCAAGTATATTGG 1397  
RESULT 7  
ID AAA54210 standard; DNA; 1425 BP.  
XX  
AC AAA54210;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE Sequence encoding trichothecene resistance polypeptide.  
XX  
KW Trichothecene resistance; resistant; crop protection; mycotoxin; fungus;  
KW wheat; maize; barley; rice; heterologous gene; transformation; Fusarium;  
KW ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
FH Key  
FT Location/Qualifiers  
FT 1..1425  
FT /\*tag= a

/product= "Trichothecene resistance polypeptide"  
WO200060061-A2.  
12-OCT-2000.  
29-MAR-2000; 2000WO-EP002769.  
31-MAR-1999; 99US-00282995.  
11-FEB-2000; 2000US-00502852.  
(NOVS ) NOVARTIS AG.  
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Hohn TM, Peters C, Salmerton JM, Reed JN, Dawson JL;  
WPI; 2000-679374/66.  
P-PSDB; AAB03936.  
Plant cell for preventing mycotoxin contamination of wheat, maize, barley  
or rice plant, comprises heterologous polynucleotide encoding gene  
product expressed in cell, having trichothecene resistance activity.  
Claim 8; Page 50-51; 62pp; English.  
A heterologous gene encoding a gene product which confers trichothecene  
resistance can be used to transform plant cells to make them resistant to  
fungal infection. The transformation method is useful for preventing  
mycotoxin contamination of a plant, particularly a crop plant such as  
wheat, maize, barley or rice, and for reducing and/or preventing the  
growth of a fungus of the genus Fusarium that produces a trichothecene,  
preferably comprising a C-3 hydroxyl group, by growing transformed crop  
plants in an area which is moderate to severe fungal infestation  
XX  
SQ Sequence 1425 BP; 431 A; 305 C; 293 G; 396 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.97e-84 Length: 1425  
Score: 962.50 Matches: 202  
Percent Similarity: 62.8% Conservative: 84  
Best Local Similarity: 44.4% Mismatches: 158  
Query Match: 41.24% Indels: 11  
DB: 3 Gaps: 8  
US-10-614-954-6 (1-451) x AAA54210 (1-1425)  
QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu 25  
Db 64 CAACCTTGATATTTTGGGACAAACACCTTCGCTATACAACTATACACTCAATATGCTCT 123  
QY 26 LeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45  
Db 124 ATCTACCGTGTACAGATCCTTCTGCTCATGACCATATCGTAATAACTTAAACAGAGA 183  
QY 46 LeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLysAlaGluGlyIle 65  
Db 184 CTTGAACATTTGGCTAAAAATTTCCAGTGGCTAGCAGGAATGTCTATAATGAAGTGTCT 243  
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgValVal 85  
Db 244 GACGAAGGTAAACATGGGTACCTACAGAAATTTGCCGTGAGCAAAATTTCCA---CTTATC 300  
QY 86 ValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105  
Db 301 GTCCAAGATCTTCGAGAAGATCTGTCTGCCCAACAATGGATTGCTTGAAGAACTGAC 360  
QY 106 TyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLysThrLeu---ProIle 124  
Db 361 TTTCTATCTACATGTTAGACGAAAGAACTTTTGGCGCTTGGCATGACTATCAATCCACT 420  
QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuGlnLeuAsnPhe 143  
Db 421 GGAAACATATAGGTATGGCGCCCAAGTGGGCTGTATTGTCAGTTTCAAGCAACTTT 480



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Db 174 CTCTGCTTTCGGTTCGATCTCATCTGATCAC---GAGATAGTCAGGACCCCTAGAGAAT 230
Qy 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 64
Db 231 GGCTCGAAGACTGCTCCACCAATTCCTGGGTAGCAGCCAGATAGTCAGTGAAGGC 290
Qy 65 IleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 84
Db 291 AGCAGCCACAACTCTGGCACATTCATGATCAAGACCTGGGAAGACTCCACCACTG 350
Qy 85 ValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAla 104
Db 351 GTTGTGAAGACTTCCGTCATGATCCGACGTTCCGACCATGACGATTTGAGACGCGCC 410
Qy 105 GlyTyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLysThrLeuProIle 124
Db 411 GACTTTCCTTTCGGATGTAGACGAGAACATATGCTCTCGGAAACCTTGCCA--- 467
Qy 125 GlyProGlyThrGlyProAspPro-----LysProValIleLeuLeuGlnLeuAsn 142
Db 468 -----AGCCCTGACGAGATATATCTCACCGGCTTCTGTGTCAGGCTAAT 515
Qy 143 PheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetVal 162
Db 516 TATATTCACGCGCGCTGCTGCTCACTCTTTGTGGCCATCATAGCACAAATGGACATGACT 575
Qy 163 GlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGlu 182
Db 576 GGTGANGGACAGGTATTCACCTTCTCTGAAGCATGTCTGGGATACATATACAGA 635
Qy 183 GluGluMetThrAlaMetAsnLeuAspArgLysThrIleValPro 197
Db 636 TTGGAGCTAGAGTCAGGGAAGTAAATGGAAGTCACTCTGTTCCC 680

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## RESULT 9

```

ADE81194
ID ADE81194 standard; DNA; 1440 BP.
XX AC ADE81194;
XX 29-JAN-2004 (first entry)
XX DE Orf11 coding sequence, SEQ ID 22.
XX KW ML-236B; HMG-CoA reducing enzyme; ds; Orf11.
XX OS Penicillium citrinum.
XX FH Key Location/Qualifiers
XX CDS 1..1440
XX FT /*tag= a
XX FT /product= "Orf11"
XX PN JP2003116567-A.
XX 22-APR-2003.
XX PF 15-OCT-2001; 2001JP-00316578.
XX PR 15-OCT-2001; 2001JP-00316578.
XX PA (SANY ) SANKYO CO LTD.
XX DR WPI; 2003-817677/77.
XX DR P-PSDB; ADE81195.
XX PT Novel DNA associated with synthesis of ML-236B, useful for improving ML-
XX PT 236B production in ML-236B producing microbe.
XX PS Example 8; SEQ ID NO 22; 142pp; Japanese.
XX OS The present invention relates to a DNA sequence (I, ADE81173), which is

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CC associated with ML-236B synthesis. (I) is useful for improving ML-236B  
 CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing  
 CC microbe. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 1440 BP; 336 A; 359 C; 367 G; 378 T; 0 U; 0 Other;

## Alignment Scores:

```

Pred. No.: 6,55e-25 Length: 1440
Score: 356.50 Matches: 129
Percent Similarity: 44.44% Conservatives: 87
Best Local Similarity: 26.54% Mismatches: 183
Query Match: 15.27% Indels: 87
DB: 10 Gaps: 20

US-10-614-954-6 (1-451) x ADE81194 (1-1440)
Qy 25 LeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGln 44
Db 58 CTGTGTTTCCCTCACTCGGATGCATCA---ATTCCGCAAACTGTTTTCAGTCTTCGGAG 114
Qy 45 GlyLeuLysArgPheSerGluAlaValProTyrValAlaGly-----GlnValLys 61
Db 115 GGACTCTCCAGGTTTATGCCAAGTTACTATTCTTCTAGGCAACCTCCAGCAAGTCGAA 174
Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleVal-----ProPhe 78
Db 175 AATGCTGGGCTCAGACCTGGA-----AGTTTCGCGTGAATCAAAACCATCC 222
Qy 79 GluAspValProArgValValValLysAspLeuArgAspProSerAlaPro----- 96
Db 223 GAGCCG---CCTACCTTTTCAGTTCGAGACATGACGAGCGGCTCTAGTACAGATTGGAGT 279
Qy 97 ---ThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIle 115
Db 280 TGGACATACCATGATCTCGTGAAAGGGGATTTCCATGAGTCTGCTGACCGGACGTT 339
Qy 116 IleAlaProArgLysThrLeuProIleGlyThrGlyProGlyProAspProLysPro 135
Db 340 CTCGCCCCG-----ACTGATCCCTGTTTCAGGGGGTACA 372
Qy 136 ValIleLeu---LeuGlnLeuAsnPheIleLysGlyLeuIleIleuThrValAsnGly 154
Db 373 AGACTCTTGGCTGCAAGCAAAATTCATTCGGGAGGCTGCCTGTTATACCTCTCAACC 432
Qy 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAla 174
Db 433 TGCACGCTTCGCGGACGCTTTCGACTCTCTACCTTGTCTATGTGAGTGGAGTCGGCAA 492
Qy 175 CysArgAsnAspProPheThrGluGluMet----- 185
Db 493 TGCCGTGATGCTCTTGGCACCAGTCACGAAATACCGAATGTTAGCAGGCAGAAAGAAAT 552
Qy 186 ---ThrAlaMetAsnLeuAsp-----ArgLysThrIleVal---ProTyrLeuGlu 200
Db 553 TCCACGGCATTGGATCAAGACTCGCCCTGTCGACGTAGTGTGTTCAACCTTATAGTCCC 612
Qy 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
Db 613 AGTCAAGCGGTCTATGAGCGTCTCAAAATCCAAACCAATTCGTGGCATGTTTGGGGTTG 672
Qy 221 Asp-----AlaValLeuThrProValSer 228
Db 673 GATTGGAGACCCAAAGAACGACGATCGGATATTGATGTCTCAGATCCCTCCGCGCT 732
Qy 229 AlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAla 248
Db 733 GTGAGGTGCTATATTCTCTATTACCCCAATTCGTGAGAGGTTGAGGCAAGTGGCT 792
Qy 249 -----ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265
Db 793 CTAGGGGGGTCTCTGGGTGTTCCAAATCTTCACAGTCTATTTCACGCGACGATCACTG 852
Qy 266 SerAlaPheIleTrpLysSerAlaSerArgValArgLeu---GluArgIleAspGlySer 284

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Db 853 GGGGCTCTGTTGGAGCTGCTTATGAGAGCTGTTGACGGAACGAAAGATTTTCGAG 912  
 QY 285 AlaProThrGlu-----PheCysArgAlaValAspAlaMetGlyValSer 302  
 Db 913 AACCCCAAGGACGCAATGATGCGCGGTCAACGTGCGCAACTCTGTCTGTCCA 972  
 QY 303 AsnAsnTyrProGly-----Leu 308  
 Db 973 GAAACACATCTTGGCAACACGATTTTATGCGGTGACAAAGCTGTCATTGATCTGCTC 1032  
 QY 309 LeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAlaAsnGluSerLeuGly 328  
 Db 1033 GCCACTAGGGGACACAGCACTTTGAATGTTGTTGCTCAGAGTTTGGCGGAATCTCTC--- 1089  
 QY 329 AlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArgThrArg 348  
 Db 1090 -----GACGAGCTGAGAGACTCTAGTATGTTTCAAGAGCGGTA 1128  
 QY 349 GlyLeuAlaThrTyrLeuHisAsnProAspLysSerAsnValSerLeuThrAlaAsp 368  
 Db 1129 GAATTTGGCA-----AACAACTCCGGATGTCGGCGCATCGGACTCTCATTTCC 1179  
 QY 369 AlaAspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyr 388  
 Db 1180 ACCTGGTTCGGGAGAACATGGTGTAGTTCTTCTCGATTGCGCTACTAGACTGG 1239  
 QY 389 AspPheGlyLeu-----GlyLeuGlyLysProGluThrValArgArgProIle 404  
 Db 1240 GATTTCGGAAGTATATCTACGGGGCTTGGGACCGGACAGATGATGATTCCTCC--- 1296  
 QY 405 PheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGluPheCys 424  
 Db 1297 GACAACTGTTTGAAGGTATAACCTTTACTATGCCCCAGCGACACGATCCTCTGAA 1356  
 QY 425 AlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThr 444  
 Db 1357 ATCATGATCACCATGAAGACAGTGGATATGGAGATATTGATACCGATCAAACCTTCACT 1416  
 QY 445 LysTyrAlaGlnTyrVal 450  
 Db 1417 GAGTCTTCAGCTTTGTA 1434

RESULT 10  
 ADE81173  
 ID ADE81173 standard; DNA; 72149 BP.  
 AC ADE81173;  
 DT 29-JAN-2004 (first entry)  
 DE ML-236B synthesis related DNA sequence, SEQ ID 1.  
 DE ML-236B; HMG-CoA reducing enzyme; ds.  
 KW ML-236B; HMG-CoA reducing enzyme.  
 OS Penicillium citrinum.  
 XX JP2003116567-A.  
 PN 22-APR-2003.  
 PD 15-OCT-2001; 2001JP-00316578.  
 PF 15-OCT-2001; 2001JP-00316578.  
 PR (SANY ) SANKYO CO LTD.  
 PA WPI; 2003-817677/77.  
 XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-236B production in ML-236B producing microbe.  
 PT Claim 1; SEQ ID NO 1; 142pp; Japanese.

XX The present invention relates to a DNA sequence (I, ADE81173), which is associated with ML-236B synthesis. (I) is useful for improving ML-236B production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing microbe.  
 XX Sequence 72149 BP; 18531 A; 17735 C; 17402 G; 18481 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,65e-22 Length: 72149  
 Score: 356.50 Matches: 129  
 Percent Similarity: 44.44% Conservative: 87  
 Best Local Similarity: 26.54% Mismatches: 183  
 Query Match: 15.27% Indels: 87  
 DB: 10 Gaps: 20

US-10-614-954-6 (1-451) x ADE81173 (1-72149)

QY 25 LeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGln 44  
 Db 24167 CTGTGTTTCCCTCACTCGGATGCATCA---ATTCCGCAAACTGTTTTCAGTCTCTCGGAG 24223  
 QY 45 GlyLeuLysArgPheSerGluAlaValProTrpValAlaGly-----GlnValLys 61  
 Db 24224 GGACTCTCAAGTTTATGCCAAGTTACTATTCTTACTGGCAACCTCCAGCAAGTCGAA 24283  
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleVal-----ProPhe 78  
 Db 24284 AATGCTGGGCTCAGACCTGGA-----AGTTTCGCGTGAATCAAAACCATCC 24331  
 QY 79 GluAspValProArgValValValLysAspLeuArgAspProSerAlaPro----- 96  
 Db 24332 GAGCCG---CCTACCCCTTTTCAGTTTCAGACATGACGAGCGGCTCTAGTACAGATTGAGT 24388  
 QY 97 ---ThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIle 115  
 Db 24389 TGGACATACCATGATCTCGTGAAACGGGATTTCCATGAGTCTGCTGACCGGAGCTT 24448  
 QY 116 IleAlaProArgLysThrLeuProIleGlyProGlyThrGlyProAspAspProLysPro 135  
 Db 24449 CTCGCCCG-----ACTGATCCCTGTTTCAGGCGGTACA 24481  
 QY 136 ValIleLeu---LeuGlnLeuAsnPheIleLysGlyGlyLeuLeuThrValAsnGly 154  
 Db 24482 AGACTCTTGGCTGCAACAGCAAAATTTTCATTCGGGAGGCTGCTGTATATACGTTCAACC 24541  
 QY 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAla 174  
 Db 24542 TCGCAGCCTTCGGGACGCGCTTTGGACTCTCTACCTTCTGTATGTGAGTGGAGTCGGCAA 24601  
 QY 175 CysArgAsnAspProPheThrGluGluMet----- 185  
 Db 24602 TGGCGTGTGCTCTTGGCACCATGACGAAATACCGAATGTTAGCAGGAGGAGAAATTT 24661  
 QY 186 ---ThrAlaMetAsnLeuAsp-----ArgLysThrIleVal---ProTyrLeuGlu 200  
 Db 24662 TCCACGGCATTTGGATCAAGACTCGCCTGTCGAGTCTAGTCTGTTCAACCTATAGTCCC 24721  
 QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 220  
 Db 24722 AGTCAGCGGTATGAGCGTCTCAAAATCCAAACCAATCTGTGGCATGTTTGGGGTTG 24781  
 QY 221 Asp-----AlaValLeuThrProValSer 228  
 Db 24782 GATTGGAGACCCAAAGAACGACGAGTCCGATATTGATGCTCTCAGATCCCTCGTGCCT 24841  
 QY 229 AlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAlaAla 248  
 Db 24842 GTGAGTCTGTGTATATTCTATTACCGCAAAATTTCTGTGAGAAAGTTGAGGCAAGTGGCT 24901  
 QY 249 -----ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265  
 Db 24902 CTAGGGGGGTCTTCTGGTGTTCAAAATCTTACAGTCTATTTCACGAGCATGACTG 24961



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QY 266 SerAlaPheIleTriPlysSerAlaSerArgValArgLeu---GluArgIleAspGlySer 284
DB 24962 GGGCCCTGCTTGGAGCTCCCTTATGAGAGCTCGTTTACGGAACGAGAACTTTCGAG 25021
QY 285 AlaProThrGlu-----PheCysArgAlaValAspAlaArgProAlaMetGlyValSer 302
DB 25022 AACCCCAAGGACGCAACATGATGCGAGCGGTCAACGTCGCGAACTCTGCTGTTCGA 25081
QY 303 AsnAsnTyrProGly-----Leu 308
DB 25082 GAAACACATCTTGGCAACACGATCTTTATGCGGTGCAAAAGCTGTCCATTGATCTGCTC 25141
QY 309 LeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAlaAsnGluSerLeuGly 328
DB 25142 GCCACTAGGGGCACACACATTGATGTGTGCTCAGAGTTGGCGGAATCTCTC--- 25198
QY 329 AlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArgThrArg 348
DB 25199 -----GACGAGCTCAGAGACTCTAGTATGTTTCAAGAGCGGTA 25237
QY 349 GlyLeuAlaThrTyrLeuHisAsnProAspLysSerAsnValSerLeuThrAlaAsp 368
DB 25238 GAATTGGCA-----AACACATCCCGGATGTCGCGGCATGGGACTCTCATTTCCC 25288
QY 369 AlaAspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyr 388
DB 25289 ACGTGGTTCGGGAGACATGTTGTTAGTTCTCTTCTCGATTGCGGCTACTAGACTGG 25348
QY 389 AspPheGlyLeu-----GlyLeuGlyLysProGluThrValArgArgProIle 404
DB 25349 GATTCGGAAGTATATCTCACGGGGGCTTGGGCAAGCCGACAGATGCGATTCGCC--- 25405
QY 405 PheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGluPheCys 424
DB 25406 GACAGTGTGTTGAAGGTATAACCTTTACTATGCCCGCAGCAGCAGCATCGTGA 25465
QY 425 AlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThr 444
DB 25466 ATCATGATCACCATGAAGACAGCTGGATATGGAGATATTGATGCCGATCAACCTTCACT 25525
QY 445 LysTyrAlaGlnTyrVal 450
DB 25526 GAGTCTTTCAGCTTTGTA 25543
RESULT 11
ABZ54817
ID ABZ54817 standard; cDNA; 482 BP.
XX
AC ABZ54817;
XX
DT 28-MAR-2003 (first entry)
XX
DE Aspergillus oryzae polynucleotide SEQ ID NO 3930.
XX
KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
XX expressed sequence tag; gene; ss.
XX
OS Aspergillus oryzae.
XX
PN WO200279476-A1.
XX
PD 10-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-IB000890.
XX
PR 30-MAR-2001; 2001JP-00098371.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (NARE-) NAT RES INST BREWING.
XX (NOR) NAT FOOD RES INST MIN AGRIC.
XX
PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
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PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
XX WPI; 2003-046817/04.
XX
PT Detection of expression of specific Aspergillus genes for monitoring the
XX fermentation and growth conditions of the fungus, using DNA probes.
XX
PS Claim 1; SEQ ID NO 3930; 48pp + Sequence Listing; Japanese.
XX
CC The invention relates to a polynucleotide having any of 6006 specific
XX sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
XX specific culture conditions including one or more of eutrophic,
XX oligotrophic, solid, early germination, alkaline, high temperature, low
XX temperature or maltose culture or polynucleotides stringently hybridising
XX to these sequences. The polynucleotides are useful for monitoring the
XX progress of fermentation and the growth conditions of a fungus,
XX especially of Aspergillus oryzae which is widely used in industrial
XX fermentation. Also monitoring for fungal contamination. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 482 BP; 131 A; 109 C; 115 G; 127 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.84e-25 Length: 482
Score: 351.00 Matches: 66
Percent Similarity: 74.56% Conservative: 22
Best Local Similarity: 55.93% Mismatches: 28
Query Match: 15.04% Indels: 2
DB: 8 Gaps: 1
XX
US-10-614-954-6 (1-451) x ABZ54817 (1-482)
QY 335 ArgSerGluLeuAspPro-----AlaSerMetArgGlnArgThrArgGlyLeuAlaThr 352
DB 3 AGAATGGCAATAGACCCGACGACGCTCTTTAAAGTCTCGCACCCGCGACGCTAGCGACA 62
QY 353 TyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThrAlaAspProSer 372
DB 63 TACATTGATCTCTCGTAGACAAATCGTCCATCTCTTCGGAGCGAGTTTCAATCCCTCG 122
QY 373 ThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeu 392
DB 123 ACGGATATTATTATGATGCTCGTGGCAAGTGTCAACTGCTATCAATTACACTTCGGATTTC 182
QY 393 GlyLeuGlyLysProGluThrValArgArgProIlePheGluProValGluSerLeuMet 412
DB 183 GGCCTTGGAAAGCCGGAGGCTGTGGACGACCGCAATTCACTCCGTTGAAGGTTGATT 242
QY 413 TyrPheMetProLysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGlu 432
DB 243 TATTTTCATGCCCAAGAGGTCTGATGGGAGATTGCTGTGTTGCTCTCTGTTACAGGAGGAG 302
QY 433 AspMetAspArgLeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyrVal 450
DB 303 GATATGGCGCGGTTGGCGCGGATGAAGAGTTTACGAGTTTGGCAATATATC 356
RESULT 12
AD070366
ID AD070366 standard; cDNA; 1508 BP.
XX
AC AD070366;
XX
DT 12-AUG-2004 (first entry)
XX
DE Barley agmatine coumaroyltransferase coding sequence.
XX
KW barley; ss; gene; agmatine coumaroyltransferase; ACT; antimicrobial;
XX pathogen resistance; enzyme.
XX
OS Hordeum vulgare.
XX
```

FH Key Location/Qualifiers  
 FT CDS 8..1327  
 FT /\*tag= a  
 FT /product= "agmatine coumaroyltransferase"  
 XX WO2004044195-A2.  
 XX PN 17  
 XX PD 27-MAY-2004.  
 XX PF 11-NOV-2003; 2003WO-EP012601.  
 XX PR 12-NOV-2002; 2002EP-00025076.  
 XX PA (RISO-) RISO NAT LAB.  
 XX PI Rasmussem S, Burhenne K, Kristensen B;  
 XX DR WPI: 2004-431667/40.  
 XX DR P-PSDB; ADO70367.  
 XX  
 XX New polynucleotide encoding a polypeptide having agmatine  
 PT coumaroyltransferase (ACT) activity, useful for establishing or enhancing  
 PT a pathogen resistance in a plant, and for producing a biopolymer.  
 XX  
 XX Claim 1; Fig 1; 11pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of the  
 CC barley agmatine coumaroyltransferase (ACT) enzyme. The sequences are  
 CC useful for the preparation of an antimicrobial compound, its precursor or  
 CC a plant protection composition, for establishing or enhancing a pathogen  
 CC resistance in a plant, and for producing a biopolymer. The present  
 CC sequence is the coding sequence of the invention.  
 XX  
 XX Sequence 1508 BP; 285 A; 484 C; 472 G; 267 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 4,68e-07 Length: 1508  
 Score: 175.00 Matches: 118  
 Percent Similarity: 36.36% Conservative: 62  
 Best Local Similarity: 23.84% Mismatches: 185  
 Query Match: 7.50% Indels: 130  
 DB: 12 Gaps: 26  
 US-10-614-954-6 (1-451) x ADO70366 (1-1508)  
 QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuSerIleTyrThr 21  
 DB 35 GCGTCAAGCCGAGTACGGCGCTCGGCTCGCTCCGGGGTGTACCCGACGTCGTC 94  
 QY 22 GlnIleSerLeuTyrProValSerAspSerGlnTyrProThrIleValSer--- 40  
 DB 95 CGCTCACCGTGCTC-----GACAAGCCCACTTCGACACGTACATCTCGGTG 142  
 QY 41 -----ThrPheGlnGlnGlyLeuLysArg 48  
 DB 143 ATCTACGCTTCCACGCGCGCGCGCCCAACGCGCTTCTCGAGCCGCGGTGGCAGA 202  
 QY 49 ---PheSerGluAlaValProTTPValAlaGlyGln-----ValLysAlaGluGly--- 64  
 DB 203 GCGCTGGTGACTACCGCGAGTGG---GCCGGCGGCTCGGCTCGACGCCAGCGCGGC 259  
 QY 65 -----IleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValPro 82  
 DB 260 CGCGCGATCTCTCAACGACGCGCGCGCTCGTGGAGCGGACGCGCGAGTGGCG 319  
 QY 83 ArgValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArg 102  
 DB 320 CTCGACAGCGCTATCGCGCTCAAG-----CCACGTCGGAG----- 355  
 QY 103 LysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThrLeu 122  
 DB 356 -----GTTCTC 361

RESULT 13

QY 123 ProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu--- 141  
 DB 362 AGCTGTCACCCC---AGCGGACGACGAGGAGCTCATGTAATCCAGGTCAAG 418  
 QY 142 AsnPheIleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161  
 DB 419 CGGTTCCGCTGCGGTGCTCTGCTGGGGTTCAACCGACGACATCGTGTCCGACGGC 478  
 QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsn-----Asp 178  
 DB 479 CGCTCCACCGCAACTTCTTCGTCGGTGGAGCCAGGCCACCGCGCGCCGCGCATCGAC 538  
 QY 179 Pro-----PheThrGluGluGluMetThrAlaMetAsn 189  
 DB 539 CCCGTCGCCGTGACGACGCTGCTTCTTCTTCCATCCCCGCGAACCGCTGCACGTCGAG 598  
 QY 190 LeuAspArgLysThrIle-----ValProTyrLeuGluAsnTyrThrIleGlyProGlu 207  
 DB 599 TAGGAGCACCGTGGGTGCGAGTTCAAGCCCTAC-----GAG 634  
 QY 208 ValAspHisGlnIleVal---LysAlaAspValAlaGlyLysAlaValLeuThrPro 226  
 DB 635 AAGGCACACGACGTTGCTGTGTCGGACGGCGACGAGGAGTGTGGTGAACAAG 694  
 QY 227 ValSerAlaSerTrpAlaPheThrPheSerProLysAlaMetSerGluLeuLysAsp 246  
 DB 695 GTGCAC-----TTTCAGCCGGAGTTTCATCTCCAAAGCTCAAGGGCG 733  
 QY 247 AlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAspAlaLeuSer 266  
 DB 734 CAGGCGTCGGCT-----GGCGGCCACGACCTCGACGACCTCGAGTCGCGTGGTG 784  
 QY 267 AlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaPro 286  
 DB 785 GCACACCTGTGGCGGACATGACGTGGCGCGC-----GGGCTCAGCGCGGGAGACC 838  
 QY 287 ThrGluPheCysArgAlaValAspAlaArgProAlaMetGly-----ValSerAsnAsn 304  
 DB 839 ACCAGCGTCGCCATCGCGTGGACGGAGCGCGGTAGCGCCGAGGTGCGCGACGGA 898  
 QY 305 TyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIle----- 322  
 DB 899 TACCGCGCAACGTATCTCTGGCGCGGCCAACCCACCGCGGGGAGCTCGTGACC 958  
 QY 323 -----AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeu----- 334  
 DB 959 AGCGCGGTCAAGCACGCGCTGGAGCTCATCAGCAGGAGGTGGCCCGGATCAACGATGGC 1018  
 QY 335 -----ArgSerGluLeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThr 352  
 DB 1019 TACTTCAAGTCTTTCATCGACTTCGCCAAC----- 1048  
 QY 353 TyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspPro--- 371  
 DB 1049 -----TCCGCGCGGTGGAGAGGAGCGGTGGTGGCGACGCGCCGCGCGGACATG 1102  
 QY 372 -----SerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAsp 389  
 DB 1103 GTGCTGAGCCCAACATCGAGGTGGACACTGGCTGCTGATCCCGTCTACGACATGGAC 1162  
 QY 390 PheGlyLeuGlyLeuGlyLysProGluThrValArgArgProIlePhe----- 405  
 DB 1163 TTTCGGCGGGGG-----CGGCCATCTTCTTCTTCATGCCCAGC 1198  
 QY 406 ---GluProValGluSerLeuMetTyrPheMetProLys---LysProAspGlyGluPhe 423  
 DB 1199 TACCTGCGGTGGAGGGTCTGCTCATCTCGTGGCTGCTTCTTGTGGCGGACGCGCGGTG 1258  
 QY 424 CysAlaLeuSerLeuArgAspGluAspMetAspArgLeuLys 438  
 DB 1259 GACGCTACGTGCCACTCTTTAGCCCGGACATGAACACCTTCAG 1303

ABX78350  
ID ABX78350 standard; cDNA; 1587 BP.

XX AC ABX78350;  
XX DT 14-APR-2003 (first entry)

XX DE Wheat stress response protein EST #6.  
XX KW Plant; ss; EST; expressed sequence tag; stress response; drought; heat;  
XX KW radiation; pathogen attack; grain flavour; disease resistance;  
XX KW peptide-methionine sulphoxide reductase; DNA repair;  
XX KW intracellular protein transport.

XX OS Triticum aestivum.  
XX PN US2002152497-A1.  
XX PD 17-OCT-2002.

XX PF 19-FEB-2002; 2002US-00078929.  
XX PR 07-MAY-1999; 99US-0133038P.  
XX PR 07-MAY-1999; 99US-0133042P.  
XX PR 11-MAY-1999; 99US-0133427P.  
XX PR 11-MAY-1999; 99US-0133428P.  
XX PR 11-MAY-1999; 99US-0133436P.  
XX PR 11-MAY-1999; 99US-0133437P.  
XX PR 11-MAY-1999; 99US-0133438P.  
XX PR 04-JUN-1999; 99US-0137667P.  
XX PR 05-MAY-2000; 2000US-00566394.

XX (FALC/) FALCO S C.  
XX PA (FAMO/) FAMODU O O.  
XX PA (MEYE/) MEYERS B C.  
XX PA (MIAO/) MIAO G.  
XX PA (ODEL/) ODELL J T.  
XX PA (RAFA/) RAFALSKI J A.  
XX PA (THOR/) THORPE C J.  
XX PA (SAKA/) SAKAI H.  
XX PA (WENG/) WENG Z.

XX PI Falco SC, Famodu OO, Meyers BC, Miao G, Odell JT, Rafalski JA;  
XX PI Thorpe CJ, Sakai H, Weng Z;  
XX DR WPI; 2003-198391/19.  
XX DR P-PSDB; ABU58179.

XX PT New peptide-methionine sulfoxide reductase and nucleic acids, useful in  
XX PT improving plant response to stress, engineering plants with increased  
XX PT disease and stress resistance, or and improving/protecting grain-flavor.

XX PS Disclosure; Page 71-72; 205pp; English.

XX CC The invention relates to isolated nucleic acids encoding plant stress  
XX CC response proteins (including peptide-methionine sulphoxide reductases)  
XX CC appearing as ABU58148-ABU58246 (or a protein 80% identical to them) from  
XX CC Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included  
XX CC are expression cassettes, transformed host cells, transgenic  
XX CC plants/seeds, modulating the level of peptide-methionine sulphoxide  
XX CC reductase in a plant and a computer system/data processing system for  
XX CC identifying, analysing, or modelling a genetic sequence. The plant  
XX CC nucleic acid is useful in developing strategies to improve plant response  
XX CC to stress (e.g. drought, heat, radiation or pathogen attack), engineering  
XX CC plants with increased disease and stress resistance, manipulating DNA  
XX CC repair and recombination efficiency, manipulating intracellular protein  
XX CC transport, and improving/protecting grain flavour. The nucleic acids may  
XX CC also be used as probes or amplification primers in the detection,  
XX CC quantitation or isolation of gene transcripts, for recombinant expression  
XX CC of encoded polypeptides, as immunogens in preparing or screening  
XX CC antibodies, and in sense or antisense suppression of one or more genes in  
XX CC a host cell, tissue or plant. The proteins may be used as immunogens or  
XX CC antigens to obtain antibodies specifically immunoreactive with the

CC protein, and in assays for enzyme agonists or antagonists. The present  
CC sequence is a plant stress response cDNA or fragment (EST, expressed  
CC sequence tag)

XX SQ Sequence 1587 BP; 287 A; 499 C; 525 G; 276 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.39e-06 Length: 1587  
Score: 170.50 Matches: 84  
Percent Similarity: 35.19% Conservative: 61  
Best Local Similarity: 20.39% Mismatches: 158  
Query Match: 7.31% Indels: 109  
DB: 10 Gaps: 15

US-10-614-954-6 (1-451) x ABX78350 (1-1587)

QY 56 ValAlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsn----- 59  
DB 275 CTGGCGGGCGCTCTGGCGGAGAGGCG-----GAGGGCGGGGTGCGATCGACTGC 328  
QY 70 ThrGlyThrSerPheIleValProPheGluAspValProArgValValValLysAspLeu 89  
DB 329 AACGGCGAGGAGCGCTCTCTCTCCGCCAGGGCGCGAGCTGCCGGGAGGACCTC 388  
QY 90 ArgAspAspProSerAlaProThrIleGluGlyMetArgLysAlaGlyTyrProMetAla 109  
DB 389 TTCGGGAGCGGTACGAGCCCTCGCGGAG---ATCAGGCGGATGTCGTGCCCTTCGCG 445  
QY 110 MetPheAspGluAsnIleAlaProArgLysThrLeuProIleGlyProGlyThrGly 129  
DB 446 -----CCTCGGCG----- 454  
QY 130 ProAspAspProLysProValIleLeuLeuGlnLeuAsnPheIleLys---GlyGlyLeu 148  
DB 455 ---GACCCGCCCTGCATATGCGCATGTTCAGGTGAGCTTCTCAAGTCGGCGGGCGG 511  
QY 149 IleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIle 168  
DB 512 GTGCTGGGCACGGGATCCACCACGTGACCATGGACGGCGTTCGCGGCTTCACATTC 571  
QY 169 ArgLeu-----LeuSerLysAlaCysArgAsnAspPro 179  
DB 572 CAGACATGACGGGTCTCGCGGGGGGTCTCCCTCTCCGAGCGGTGCCGTCGCGCGCG 631  
QY 180 PheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeu 199  
DB 632 TTCACAGCCGACGCTCTCCGCGCGGGTCCGCGCGG----- 673  
QY 200 GluAsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 219  
DB 674 -----CCGGAATTCGAGCACCCCGGTGTACTCGCGCGCGGTACCTCAAC 715  
QY 220 GlyAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLys 239  
DB 716 GGC-----GCCCGCAGCGCCCTTGTCTACCCCGGTCTACTCTCGTGTCCAGAG 763  
QY 240 AlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheVal 259  
DB 764 CTCCTCGCGGACATCAAGTCCGCGGCGCGCTGCG-----GTG 802  
QY 260 SerThrAspAspAlaLeuSerAlaPheIleTrpLys----- 271  
DB 803 TCCACTACGGCGCGGTGACCGCGCACCTCTGGCGCTGCTGTGCGCGCGCGGCTC 862  
QY 272 -----SerAlaSerArgValArgLeu-----GluArgIleAspGly 283  
DB 863 GTCGCGGCTCGACACCGCGCTCCGGTGGCGGCCAACATCCGCGACCGCTCGCGCGCG 922  
QY 284 SerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyValSerAsn 303  
DB 923 CAGCTCCCGCGCGAGTCTCTCGGCAACCCATCGTGGCGCGGACCTCGTCAACGTCAAG--- 979  
QY 304 AsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIleAla 323



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PR	18-AUG-1999;	99US-0149426P.	Db		
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PR	23-AUG-1999;	99US-0149902P.	Db		
PR	23-AUG-1999;	99US-0149930P.	QY		
PR	25-AUG-1999;	99US-0150566P.	Db		
PR	26-AUG-1999;	99US-0150884P.	QY		
PR	27-AUG-1999;	99US-0151065P.	Db		
PR	27-AUG-1999;	99US-0151066P.	QY		
PR	27-AUG-1999;	99US-0151080P.	Db		
PR	30-AUG-1999;	99US-0151303P.	QY		
PR	31-AUG-1999;	99US-0151438P.	Db		
PR	01-SEP-1999;	99US-0151930P.	QY		
PR	07-SEP-1999;	99US-0152363P.	Db		
PR	10-SEP-1999;	99US-0153070P.	QY		
PR	13-SEP-1999;	99US-0153758P.	Db		
PR	15-SEP-1999;	99US-0154018P.	QY		
PR	16-SEP-1999;	99US-0154039P.	Db		
PR	20-SEP-1999;	99US-0154779P.	QY		
PR	22-SEP-1999;	99US-0155139P.	Db		
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PR	24-SEP-1999;	99US-0155659P.	Db		
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PR	05-OCT-1999;	99US-0157753P.	Db		
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PR	21-OCT-1999;	99US-0160741P.	Db		
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PR	21-OCT-1999;	99US-0160814P.	Db		
PR	21-OCT-1999;	99US-0160815P.	QY		
PR	22-OCT-1999;	99US-0160980P.	Db		
PR	22-OCT-1999;	99US-0160981P.	QY		
PR	22-OCT-1999;	99US-0160989P.	Db		

QY	36	ProThrIleValSerThrPhe-----GluGlnGlyLeuLysArg---PheSerGluAla	52
Db	182	CCACCGCGCTTCCAATTCTTTCACCTCAGGTCATGAGGAAGCTCTTTCCAAAGCC	241
QY	53	---ValProTrp-----ValAlaGlyGlnValLysAlaGluGly-----	64
Db	242	CTTGTCCTTTTACCTATGCTGCTGCTGAAGAGACGATGATGCTGCTATTGAG	301
QY	65	IleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal	84
Db	302	ATCGATTGTACGGTCCGGTCTCTTCGTTGTT-----GCTGATACTCTCTCTGTT	355
QY	85	ValValLysAspLeuArgAspAsp-----ProSerAlaProThrIleGluGlyMetArg	102
Db	356	ATC-----GATGATTTGTTGTTGATTTGCTCTCCCTACCCCTT-----	388
QY	103	LysAlaGlyTyPzProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThrLeu	122
Db	389	-----AATCTC-----CGTCAGCTTATT	406
QY	123	Pro---IleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu	141
Db	407	CCCGAAGTTGATCACTCCACCGCATTCACCTCT---TTCCCGCTTCTCGTTTTCAGGTG	463
QY	142	AsnPheIleLys---GlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp	160
Db	464	ACTTTCTTTAAATGGGGGAGCTTCACCTTGGGGTGGGATCGACATCACGGCGCAGAT	523
QY	161	MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe	180
Db	524	GGTTTCTCTGGTCTTCATTTTATCAACACATGCTGCTGATATGGCTCGT-----	571
QY	181	ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu	200
Db	572	-----GGTCTTGAC-----	580
QY	201	AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAla-----	215
Db	581	CTAACCATTCACCTTTTCAATTGATCGAACACACTCTCCGAGCTAGGACCGCCACAG	637
QY	216	-----AspValAlaGlyGlyAsp	221
Db	638	CCTGCTTTTTCATGTTGAATATCAGCTCGCCACCAAGTATGAAGATCCCTCTTGATCCA	697
QY	222	AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet	241
Db	698	TCCAAATCAGGACCTCAGAATACACCGCTGTCTATATTCAAAATTAACACGACGACCGCTT	757
QY	242	SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr	261
Db	758	GTTGCTCTCAAA-----CCGAATCCAGGAGGATGGGAACACTGTGCTAGCTATAGCTCA	811

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DB 812 TATGAGATGTTGCAGCCCATGTTGGAGATCAGTGGAAAGCGCGA-----GGGCTT 865
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAla-----ArgPro 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 866 CCAACGACCAAGAGAGAACTGTACATTGCACTGATGGAAGGCTAGACTGCGTCCG 925
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 AlaMetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSer 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 926 CAGCTGCCT-----CCTGGTTACTTTGGGAATGTATATCTCACTGCAACA 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 ThrIle-----GlyGluIle 322
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 971 CCATTGGCTGTTGCAGGGGATCTCTATCTAAACCAACATGGTATGCTGCAGGACAGATT 1030
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 323 AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSer 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1031 CATGATTTCTGTTGTTGATGGATGATACTATCTGAGGTCAGCTCTTGAC----- 1081
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 MetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsn 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1082 -----TACCTGGAGATGCAGCCTGATCTGTCAAGC 1111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 363 ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLys 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1112 CTTGTCGGCGGTGCACATACCTACAAGTGTCCAAATTTAGGAATCAAGCTGGGTCA 1171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 383 ValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArgArg 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1172 TTACCTATTATGATGCAGACTTTGGTTGGGGT-----CGT 1207
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QY 403 ProIlePheGlu-----ProValGluSerLeuMetTyrPheMetProLys 417
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DB 1208 CCTACTTTATGGGACCTGTTGGGAATTCGTATGAGGGTTGTCGTTGTGCTACCACT 1267
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QY 418 LysPro----AspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMet 434
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AAC49441
ID AAC49441 standard; DNA; 1593 BP.
XX
AC AAC49441;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 61174.
XX
KW Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126364P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
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PR 30-APR-1999; 99US-0132048P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
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PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
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PR 13-JUL-1999; 99US-0143542P.
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PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
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QY 216 -----AspValalaGlyGlyAspAla 222
Db 638 GCTTTTCATCATGTTGAATATCAGCTGCACCAAGTATGAAGATACCTCTTGATCGCTCT 697
QY 223 ValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMetSer 242
Db 698 AAATCAGGACCTGAGAAATACCACTGCTCTATTTCAAATTAACACGAGACGAGCTTGT 757
QY 243 GluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAsp 262
Db 758 GCTCTTAAG-----CGGAATCCAGGAGGATGGGACACTGTCAGCTACAGCTCATAC 811
QY 263 AspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAsp 282
Db 812 GAGATGTTGGCAGGCGATGTTGGAGATCAGTGGGAAAGGCGCA-----GGGCTTCCA 865
QY 283 GlySerAlaProThrGluPheCysArgAlaValAspAla-----ArgProAla 298
Db 866 AAGACCAAGAGACGAAACTGTACATTGCAACTGTGAAGGTCTAGACTACGTCCGCAG 925
QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThr 318
Db 926 CTGCCT-----CCTGGTTACTTGGGAATGTGATATTCTACTGCAACACCA 970
QY 319 Ile-----GlyGluIleAla 323
Db 971 TTGGCTGTTGAGGGGATTGTTTATCTAAGCCAACATGGTATGCTGCAGGACAGATTTCAT 1030
QY 324 AsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMet 343
Db 1031 GATTTCTTGGTTCGTATGGATGATAACTATCTGAGGTCAGCTCTTGAC-----1078
QY 344 ArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsnVal 363
Db 1079 -----TACCTGGAGATGCAGCCTGATCTGTGAGCCCTT 1111
QY 364 SerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLysVal 383
Db 1112 GTCCGCGGTGCATACCTACAGTCCCAATTTGGGAATCACAAGCTGGGTAGATTGA 1171
QY 384 GlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArgArgPro 403
Db 1172 CCTATTATGATGCAGACTTGGTGGGT-----CGTCCT 1207
QY 404 IlePheGlu-----ProValGluSerLeuMetTyrPheMetProLysLys 418
Db 1208 ATCTTTATGGGACCTGGTGAATTCCATACGAGGGTTTGTCTTTGTGCTACCAAGTCCT 1267
QY 419 Pro---AspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMet 434
Db 1268 ACTAATGATGGCAGCTTATCCGTTGCCATTGCCCTCCCAATCTGAACACATG 1318
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Job time : 748 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 24, 2005, 01:46:06 ; Search time 4360 Seconds  
(without alignments)  
3769.339 Million cell updates/sec

Title: US-10-614-954-6  
Perfect score: 2334  
Sequence: 1 MAFKIQDTLQGLLSIY.....EDMDRLKADKWKYAYVG 451

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DRV=xlh  
-O=/cpn2.1/USPTO spool\_h/US10614954/runat 19012005 171527 25189/app query.fasta\_1.647  
-DB=EST-QFMR-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10614954 @CGN 1.1 3437 @runat 19012005 171527 25189 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hcc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gssi.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1132	48.5	899	4	BI949616
2	704	30.2	512	4	BI191800
3	694	29.7	508	4	BI191865
4	672	28.8	498	4	BI200717
5	648	27.8	1055	4	BI947129
6	644	27.6	499	4	BI191678
7	601	25.7	481	4	BI191864
8	576	24.7	546	2	BF253868
9	569.5	24.4	411	4	BI187781

C	10	555	23.8	448	4	BI201068
C	11	548	23.5	514	4	BI192008
C	12	543	23.3	457	4	BI187780
C	13	530.5	22.7	392	4	BI192452
C	14	530	22.7	518	4	BI191997
C	15	526	22.5	423	4	BI192498
C	16	506.5	21.7	374	4	BI187896
C	17	490	21.0	401	4	BI188598
C	18	490	21.0	401	4	BI192451
C	19	490	21.0	490	4	BI201353
C	20	484	20.7	393	4	BI188605
C	21	478	20.5	372	4	BI192380
C	22	469	20.1	348	4	BI191129
C	23	468	20.1	476	4	BI192381
C	24	459	19.7	358	4	BI201146
C	25	456.5	19.6	336	4	BI191040
C	26	451	19.3	350	4	BI190499
C	27	447	19.2	459	4	BI187539
C	28	429	18.4	330	4	BI191128
C	29	413	17.7	435	4	BI187304
C	30	405	17.4	318	4	BI192335
C	31	392	16.8	303	4	BI189964
C	32	392	16.8	304	4	BI190847
C	33	392	16.8	308	4	BI188363
C	34	392	16.8	308	4	BI190145
C	35	385	16.5	311	4	BI200611
C	36	383	16.4	303	4	BI188705
C	37	370	15.9	385	4	BI189867
C	38	340	14.6	270	4	BI188630
C	39	338	14.5	841	9	CNS060HK
C	40	336	14.4	278	4	BI191799
C	41	323	13.8	260	4	BI191495
C	42	323	13.8	352	4	BI188631
C	43	323	13.8	352	4	BI201565
C	44	323	13.8	360	4	BI187939
C	45	323	13.8	361	4	BI201147

ALIGNMENTS

BI949616 899 bp mRNA linear EST 19-OCT-2001  
HVSME10014017f Hordeum vulgare spike EST library HVCDNA0012  
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone  
HVSME10014017f, mRNA sequence.

BI949616 GI:16291032

EST.

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 899)

Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R.,

Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M.,

Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W.,

Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource

for barley genomics: Fusarium infected Morex spike cDNA library

Unpublished (2001)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 598

Seq primer: AATTACCTCTACTAAGGG

High quality sequence stop: 755.

Location/Qualifiers

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source
1. .899
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSME10014017f"
/tissue_type="Spike"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected)"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton,
Malatras). Phagemids were plated and picked at the
Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
Oates, Rambo, Main). The sequence has been trimmed to
remove vector sequence and contains a minimum of 100 bases
of phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

ORIGIN

Alignment Scores:
Pred. No.: 3,56e-113 Length: 899
Score: 1132.00 Matches: 243
Percent Similarity: 92.11% Conservative: 2
Best Local Similarity: 91.35% Mismatches: 19
Query Match: 48.50% Indels: 6
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI949616 (1-899)

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DB 110 ATGGCTTTCAGATACAGCTCGACACCTCGGCAGCTACCGGCTCTTCGATCTAC 169
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSer 40
DB 170 ACCCAATCATGCTCTCTACCGGCTCTGATCTCTCAATATCCCATATTGTGACG 229
QY 41 ThrPheGlnGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnVal 60
DB 230 ACCTTCAGGCAAGGCTTTAAGCGCTTCTCCAGAGCGCTCCATCGGTGCGAGCCAGGTC 289
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80
DB 290 AAGCCGAGGCGATTACCGAGGGAACACAGGAATCTCTTCGTCCTCTTTTGGAGGAC 349
QY 81 ValProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100
DB 350 GTTCTCTCGTGTGTAGTGAAGACCTCCGCGATGATCTCTTCAGACCCAGCGAGGT 409
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleLeuAlaProArgLys 120
DB 410 ATGAGAAAGGGGATACCTTATGGCGATGTTTGACGAGAACATCATCGGCCCCAGGAG 469

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121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuGln 140  
470 ACGTTTACCTATTGGACCTGGTACTGGTCCGACGACCCAAAGCCTGTATTTCTATTGCAG 529

141 LeuAnpPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
530 CTCACATTTTCATCAAGGCGGACTCATCTCTACTCTCCAGGCGTGGCGTAACGCCATTC 649

161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180  
590 ATGGTAGGCAAGATGCGGTGATCGCTACTCTCCAGGCGTGGCGTAACGCCATTC 649

181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrIleGlu 200  
650 ACCGAAGAAGAAATGACGCGCATGAACTCGATCGCAAGAACGATAGTTCTTTACCTTGA- 708

201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAla-GlyGln 220  
709 AACTATAGATTGGCCCGGAGTAGATCATCATGATTGCAACCTGATGATGCTGGTGG 768

220 YAspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAl 240  
769 GTGACGCTGCTTCACGCGGTCAGTGCAAGCTGGGCGCTTTCACATTCAGCCCCAG-GC 827

240 aMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSe 260  
828 CATGTCAAGCTCAG-GATGCTGTCTACCAAGACTCTGAGCATCAAC---AAAGTCGTGTC 883

260 rThrAspAlaLeu 265  
884 -ACTGACGATGCTCTT 898

RESULT 2  
BI91800  
LOCUS  
DEFINITION  
512 bp mRNA linear EST 10-JUL-2001  
12flifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone 12flifs 5', mRNA  
sequence.  
BI91800  
VERSION  
BI91800.1 GI:14665479  
KEYWORDS  
EST.  
Fusarium sporotrichioides  
Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
REFERENCE  
1 (bases 1 to 512)  
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,  
Beremand, W. and Roe, B.  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Other ESTs: 12flifs.f1  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
871 8e-94 gi|4379882|gb|AAD197 (AF121716)  
trichothecenes-0-acetyltransfer  
Seq primer: T3  
High quality sequence stop: 476.  
Location/Qualifiers  
1. .512  
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/mol\_type="mRNA"  
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/clone="12flifs"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
cDNA library"

source

/note="Vector: pBlueScript SK-; Site\_1: EcoRI; Site\_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

## ORIGIN

Alignment Scores: 1.4e-66 Length: 512  
Pred. No.: 704.00 Matches: 131  
Score: 704.00  
Percent Similarity: 89.70% Conservative: 17  
Best Local Similarity: 79.39% Mismatches: 17  
Query Match: 30.16% Indels: 0  
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191800 (1-512)

QY 2 AlaPheyleGlnLeuAsePThrLeuGlyGlnLeuProGlyLeuLeuSerlleTyThr 21  
Db 17 TCITTTTGACATAGAGCTCGACATCGCGGCAGAACCGCTCTTTTCAATCTACAC 76  
QY 22 GlnleSerLeuLeuTyProValSerAspSerGlnTyProThrleValSerThr 41  
Db 77 CAGATCAGTCTCTGTACCCCGCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC 136  
QY 42 PheGluGlnGlyLeuTyArgPheSerGluAlaValProTTPValAlaGlyGlnVallys 61  
Db 137 CTTGAGGAGGCTAAACCGCTCTCTCAACCTTCCCATGGTCGCGGCAGGTCAG 196  
QY 62 AlaGluGlyleSerGluGlyAseThrGlyThrSerPheileValProPheGluAseVal 81  
Db 197 ACCGAGGGCATGACGGAAGAAACACAGAACTTCCAAGATCAATCCATATGAGGAGA 256  
QY 82 ProArgValValVallysAsePLeuArgAsePProSerAlaProThrleGluGlyMet 101  
Db 257 CCCCCTGTGTGTGAAGACCTCCGTGATGATTCCTCAGCGCAACGATCGAGGGTTG 316  
QY 102 ArgLyAlaGlyTyProMetAlaMetPheAsePgluAseNlleleAlaProArgLyThr 121  
Db 317 AGAAGCGCGGTTCGCCCTTAGAGATGTTTGACGAGAACGTCGCTCGAGGAGAGA 376  
QY 122 LeuProileGlyProGlyThrGlyProAsePProlyseProValleleLeuLeuGln 141  
Db 377 TTAGCTATCGGAGCTGCGCAATGCCCCACGACGCGCAAGCCTGTGTGTATTCGAGCTC 436  
QY 142 AsnPhelleysGlyGlyLeulleLeuThrValAseNlyGlnHisGlyAlaMetAseMet 161  
Db 437 AACTTCATTAAAGCGGAGCTATCTCACCCTCAACGCAACATGGTGTATGGACATG 496  
QY 162 ValGlyGlnAseAla 166  
Db 497 ACAGGACAGATGCT 511

## RESULT 3

BI191865  
LOCUS  
DEFINITION  
13b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 13b10fs 5', mRNA sequence.

ACCESSION BI191865

VERSION BI191865.1

KEYWORDS GI:14665544

SOURCE EST.

ORGANISM Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 508)

Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A.,

Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished (2001)

Other\_ESTs: 13b10fs.fl

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 857 3e-92 gi|4378882|gb|AAD197 (AF127176) trichothecenes-3-O-acetyltransferase  
Seq primer: T3  
High quality sequence stop: 450.

## FEATURES

## source

1..508  
Location/Qualifiers  
/organism="Fusarium sporotrichioides"  
/mol\_type="mRNA"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
/clone="13b10fs"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"  
/note="Vector: pBlueScript SK-; Site\_1: EcoRI; Site\_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.72e-65 Length: 508  
Score: 694.00 Matches: 129  
Percent Similarity: 89.09% Conservative: 18  
Best Local Similarity: 78.18% Mismatches: 18  
Query Match: 29.73% Indels: 0  
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191865 (1-508)

QY 2 AlaPheyleGlnLeuAsePThrLeuGlyGlnLeuProGlyLeuLeuSerlleTyThr 21  
Db 14 TCTTTTGACATAGAGCTCGACATCATCGCGGCAGAACCGCTCTTTTCAATCTACAC 73  
QY 22 GlnleSerLeuLeuTyProValSerAspSerGlnTyProThrleValSerThr 41  
Db 74 CAGATCAGTCTCTGTACCCCGCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC 133  
QY 42 PheGluGlnGlyLeuTyArgPheSerGluAlaValProTTPValAlaGlyGlnVallys 61  
Db 134 CTTGAGGAGGCTAAACCGCTCTCTCAACCTTCCCATGGTCGCGGCAGGTCAG 193  
QY 62 AlaGluGlyleSerGluGlyAseThrGlyThrSerPheileValProPheGluAseVal 81  
Db 194 ACCGAGGGCATGACGGAAGGAGACACAGAACTTCCAAGATCAATCCATATGAGGAGA 253  
QY 82 ProArgValValVallysAsePLeuArgAsePProSerAlaProThrleGluGlyMet 101  
Db 254 CCCCCTGTGTGTGAAGACCTCCGTGATGATTCCTCAGCGCAACGATCGAGGGTTG 313  
QY 102 ArgLyAlaGlyTyProMetAlaMetPheAsePgluAseNlleleAlaProArgLyThr 121  
Db 314 AGAAGCGCGGTTCGCCCTTAGAGATGTTTGACGAGAACGTCGCTCGAGGAGAGA 373  
QY 122 LeuProileGlyProGlyThrGlyProAsePProlyseProValleleLeuLeuGln 141  
Db 374 TTAGCTATCGGAGCTGCGCAATGCCCCACGACGCGCAAGCCTGTGTGTATTCGAGCTC 433  
QY 142 AsnPhelleysGlyGlyLeulleLeuThrValAseNlyGlnHisGlyAlaMetAseMet 161  
Db 434 AACTTCATTAAAGCGGAGCTATCTCACCCTCAACGCAACATGGTGTATGGACATG 493  
QY 162 ValGlyGlnAseAla 166  
Db 494 ACAGGACAGATGCA 508

## RESULT 4

```

BI200717      498 bp mRNA linear EST 10-JUL-2001
LOCUS         ole06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION    library Fusarium sporotrichioides cDNA clone ole06fs 5', mRNA
sequence.
ACCESSION     BI200717.1 GI:14666689
VERSION       Fusarium sporotrichioides
KEYWORDS      EST.
SOURCE        Fusarium sporotrichioides
ORGANISM      Fusarium sporotrichioides
REFERENCE     Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
AUTHORS       Beremand,M. and Roe,B.
TITLE         Analysis of a Fusarium sporotrichioides EST database
COMMENT       Unpublished (2001)
CONTACT       Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
DEPARTMENT    Department of Chemistry and Biochemistry
INSTITUTION   Advanced Center for Genome Technology, University of Oklahoma
ADDRESS       620 Parrington Oval, Norman, OK 73019, USA
TEL           Tel: 405 325 4912
FAX           Fax: 405 325 7762
EMAIL         Email: broe@ou.edu
NOTE          Contact Dr. Marian Beremand regarding clone availability Included
              is the best homolog from a blastx search of Genbank nr 04-09-01
              743 8e-79 gi|4378982|gb|AAD197 (AF127176)
              trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.
FEATURES      1. .498
              Location/Qualifiers
                source          BB
                organism        "Fusarium sporotrichioides"
                mol_type        "mRNA"
                strain          "Tri 10"
                db_xref          "taxon:5514"
                clone            "ole06fs"
                cDNA_library     "Fusarium sporotrichioides Tri 10 overexpressed
                cDNA library"
                notes            "Vector: pBluescript SK-; Site 1: EcoRI; Site_2:
                XhoI; 5' end of cDNA cloned into EcoRI site of
                pBluescript; 3' end of cDNA cloned into XhoI site of
                pBluescript"

ORIGIN
Alignment Scores:
Pred. No.:      3,83e-63      Length:      498
Score:          672.50        Matches:     130
Percent Similarity: 86.75%    Conservative: 14
Best Local Similarity: 78.31% Mismatches:     21
Query Match:    28.81%      Indels:       1
DB:             4            Gaps:       1

US-10-614-954-6 (1-451) x BI200717 (1-498)

QY      149  ILeLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIle 168
DB      3  ATTCTCACCGTCAACGACACATGGTGTATGACATGACAGGACAGCAAGATGCAATTATT 62
QY      169  ArgLeuLeuSerLysAlaCysArgAsnAspPropheThrGluGluGluMetThrAlaMet 188
DB      63  CGTCTTCTCTCCAAAGCGTCCGCCAACGAATCATTCACCGAGAGAGAAATCTCGGCCATG 122
QY      189  AsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThrIleGlyProGluVal 208
DB      123  AACCTCGATCGCAAGCGGTAGTCCCTCTCTTGAAACTACAAAGTTGGTCTCTGAGCTA 182
QY      209  AspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrProValSer 228
DB      183  GACCACCAAGATGCCAAACCTGGCGCTGCT---GGCGACGCTCCACCCGACCGGCCAAG 239
QY      229  AlaSerTrpAlaPheThrPheSerProLysAlaMetSerCluLeuLysAspAlaAla 248

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DB      240  GCAAGCTGGCGCTCTTTTCATCTACTCCCAAGGCCCTCTCGAGCTGAAAGACGACGCC 299
QY      249  ThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAspAlaLeuSerAlaPhe 268
DB      300  ACAAGAGACTCTTGACGCGTGGTCCCAAGTTTGTGTCAACTGATGATGCTCTTTTCGGCGTTT 359
QY      269  IleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaProThrGlu 288
DB      360  ATCTGGCAATCAACCTCGCGGTAGCTCTCGCAGATTGGATGTTCCACACTACTGAA 419
QY      289  PheCysArgAlaValAspAlaArgProAlaMetGlyValSerAsnAsnTyrProGlyLeu 308
DB      420  TTCTCCGCGCTGTGCATGCGGGGCCCAATGGCGGTATCAAGCACATACCAGGCCTT 479
QY      309  LeuGlnAsnMetThrTyr 314
DB      480  CTTCAAAACATGACCTAC 497

RESULT 5
LOCUS    BI947129
DEFINITION
HVSME1003N10f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME1003N10f, mRNA sequence.
ACCESSION BI947129
VERSION    BI947129.1 GI:16286403
KEYWORDS
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
REFERENCE  1 (bases 1 to 1055)
AUTHORS    Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R.,
            Heinen,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M.,
            Rambo,T., Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W.,
            Gates,R. and Main,D.
            Development of a genetically and physically anchored EST resource
            for barley genomics: Fusarium infected Morex spike cDNA library
            Unpublished (2001)
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hg bases = 147
            Seq primer: AATTAACTCTCACTAAAGG
            High quality sequence start: 5
            High quality sequence stop: 668.
FEATURES   1. .1055
            Location/Qualifiers
              organism="Hordeum vulgare subsp. vulgare"
              mol_type="mRNA"
              cultivar="Morex"
              sub_species="vulgare"
              db_xref="taxon:112509"
              clone="HVSME1003N10f"
              tissue_type="Spike"
              lab_host="TJC121"
              (Fusarium infected)
              /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site_2:
              XhoI; Plants were grown at the University of Minnesota in
              the GJ Muehlbauer lab; spikes were harvested and snap
              frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
              graminearum inoculation (Heinen). In the TJ close lab at
              the University of California, Riverside, total RNA was
              prepared from each sample pool, equal quantities of all
              eight RNA pools were combined, poly(A) RNA was purified
              from the mixture, one primary unamplified cDNA library was
              made, and 1 million pfu were in vivo excised to give

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Db      258 TGGGCCAAGTGGGAGTCTCGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCTGAGAGT 199
QY      400 ValArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysPro 419
Db      198 GTGAGAGAGACTCGCTTTGAACCTTTTGAGAGTTTGATGACCTTTATGCCAAGAAGCCT 139
QY      420 AspGlyGluPheCysAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAla 439
Db      138 GATGGGAGTTTACGGCGTCCATTCTCTGAGGAGTGGAGATATGAGAGACTAAAGGCG 79
QY      440 AspLysGluTrpThrLysTyrAlaGlnTyrValGly 451
Db      78 GATGAGAGTGGCAAAAGTACGCAAAAGTATATTGGG 43

RESULT 7
LOCUS   BI191864/c 481 bp mRNA linear EST 10-JUL-2001
DEFINITION
Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 13b10fs 3', mRNA
sequence.
ACCESSION BI191864
VERSION BI191864.1 GI:14665543
KEYWORDS
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE
1 (bases 1 to 481)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other ESTs: 13b10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
745 4e-79 gi/4378882[gbl/AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 340.
FEATURES
source
1. .481
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="13b10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
pBluescript"
ORIGIN
Alignment Scores:
Pred. No.: 2,54e-55 Length: 481
Score: 601.00 Matches: 110
Percent Similarity: 90.85% Conservative: 19
Best Local Similarity: 77.46% Mismatches: 13
Query Match: 25.75% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191864 (1-481)
QY      310 GlnAsnMetThrTyrHisSerThrIleGlyGluIleAlaAsnGluSerLeuGlyAla 329

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Db      479 CAAAACATGACCTACCATGACTCGACCGTCGCCGAAATCCCAACGACCACTTGGCGCA 420
QY      330 ThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArgThrArgGly 349
Db      419 ACAGCATACGCTGCGCTCGGAACCTCAACAGTGATCGTTTGGCGAGAGAACACAAAGCT 350
QY      350 LeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThrAlaAspAla 369
Db      359 TTGGCGACGTACATGATGCGCTGCGCTGACAAAGTCGAGCGTCTCCCTGACCGCGGATGCG 300
QY      370 AspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAsp 399
Db      299 AATCCGTCGAAGCAGCATCATGCTGAGTTCTCTGGGCCAAGGTGGGATGCTGGGAGTATGAC 240
QY      390 PheGlyLeuGlyLysProGluThrValArgAtgProIlePheGluProValGlu 409
Db      239 TTGGGTTTGGAGTGGGTAAAGCTGAGAGTGAGAGACCTCGCTTTCGACCTTTTGAG 180
QY      410 SerLeuMetTyrPheMetProLysLysProAspGlyGluPheCysAlaLeuSerLeu 429
Db      179 AGTTTGATGTACTTTATGCCCAAGAGCCTGATGGGAGTTTACGGCGTCCATTCTTTG 120
QY      430 ArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyr 449
Db      119 AGGGATGAGGATATGGAGAGACTAAAGGCGGATGAGAGTGGACAAAGTACGCAAGTAT 60
QY      450 ValGly 451
Db      59 ATTGGG 54

RESULT 8
LOCUS   BF253868
DEFINITION
546 bp mRNA linear EST 23-OCT-2001
HVSMEF0002F13f Hordeum vulgare seedling root EST library HVCNA0007
(Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEF0002F13f, mRNA sequence.
ACCESSION BF253868
VERSION BF253868
KEYWORDS
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
REFERENCE
1 (bases 1 to 546)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Yu,X., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
COMMENT On Nov 16, 2000 this sequence version replaced gi:11182973.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 376
Seq primer: AATTAACCTCTACTAAAGG
High quality sequence stop: 532.
FEATURES
source
1. .546
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEF0002F13f"
/tissue_type="Seedling root"
/lab_host="TJCI21"
/clone_lib="Hordeum vulgare seedling root EST library

```

HVCDNA007 (Etiolated and unstressed)"  
/notes=vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
Seeds were surface sterilized then germinated under axenic  
conditions in the dark at room temperature on filter paper  
with water, nystatin and cefotaxime in covered  
crystallization dishes. Five-day old seedling roots were  
then harvested, total RNA was prepared, poly(A) RNA was  
purified, one primary unamplified cDNA library was made,  
and 1 million pfu were in vivo excised to give pluescript  
SK(-) cDNA phagmids. These steps were performed in the TJ  
Close laboratory at the University of California,  
Riverside (Choi, Close, Fenton). Phagemids were plated and  
picked at the Clemson University Genomics Institute (CUGI)  
(Segum, Palmer, Frisch, Atkins and Wing). Plasmid DNA  
preparations, DNA sequencing and sequence analysis were  
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,  
Oates, Rambo, Main). The sequence has been trimmed to  
remove vector sequence and contains a minimum of 100 bases  
of phred value 20 or above. For more details on library  
preparation and sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders> Also  
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,71e-52 Length: 546  
Score: 576.00 Matches: 105  
Percent Similarity: 79.43% Conservative: 34  
Best Local Similarity: 60.00% Mismatches: 34  
Query Match: 24.68% Indels: 2  
DB: 2 Gaps: 1

US-10-614-954-6 (1-451) x BF253868 (1-546)

QY 277 ArgLeuGluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArg 296  
DB 1 CGTCTTCCGTTAGAGNATCGGCCGACTCTATTCTGCGCGCGCTCGACGTCGA 60  
QY 297 ProAlaMetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsn 316  
DB 61 ACCAGCTTGATGTGCCAAGCACTACCTCGCATTCCTCAGAACATGGCCTACAGCA 120  
QY 317 SerThrIleGlyLeuIleAlaGluSerLeuGlyAlaThrAlaSerArgLeuArgSer 336  
DB 121 TCAACCTGTCTCAATAGCAATGAGCCCTTGGGTATTGTGGCCACTCGTCTACGAGCC 180  
QY 337 GluLeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356  
DB 181 CAACTTGACCGCGAGTCTCTCGACGCTCGACACAGCCCTTTGTTTCACATAGCTAA 240  
QY 357 AsnProAspGlySerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376  
DB 241 CATCCCT-----GGTACTTGTCTGTACAGCAGATGCCAATCCGCTACTGATATTATG 294  
QY 377 LeuSerSerTrpAlaValGlyLeuTrpAspTyrAspPheGlyLeuGlyValGly 396  
DB 295 TTGAGCTCTTGGGCCAAGACCGGATCGTGGAACCTATGACTTTGGTCTTGGGCTGGGAA 354  
QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416  
DB 355 CTGAGAGCGTAAGAGACCGATCTTTGAGCCTATGAGAGTTTGATGATCTTATGCC 414  
QY 417 LysLysProAspGlyGluPheCysAlaLeuSerLeuArgAspGluAspMetAspArg 436  
DB 415 AAGAGACCAAGATGAGAAATTAAGTCTGCTTGGCTTTGAGACGAGGATATGGAGATT 474  
QY 437 LeuLysAlaAspGlyGluTrpThrLysTyrAlaGlnTyrValGly 451  
DB 475 TTGAAGAGCGATGAGAAGTGGAGAAATTTGGACCGCTTCATCGGA 519

## RESULT 9

BI187781

## LOCUS

## DEFINITION

BI187781 411 bp mRNA linear EST 10-JUL-2001  
b2d04fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA  
sequence.

## ACCESSION

BI187781

## VERSION

BI187781.1

## KEYWORDS

GI:14661460

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1. 411

## /organism="Fusarium sporotrichioides"

## /mol\_type="mRNA"

## /strain="Tri 10"

## /db\_xref="taxon:5514"

## /clone="b2d04fs"

## /cna\_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

## /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

## Alignment Scores:

Pred. No.: 5,73e-52 Length: 411

Score: 569.50 Matches: 110

Percent Similarity: 89.78% Conservative: 13

Best Local Similarity: 80.29% Mismatches: 13

Query Match: 24.40% Indels: 1

DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI187781 (1-411)

QY 135 ProValIleLeuLeuGlnLeuAsnPheIleGlyGlyLeuIleThrValAsnGly 154

DB 3 CTGTGTTGCTATTGAGCTCAACTTCATTAGGCGGACTCATTTCTACCGTCAACGGA 62

QY 155 GlnHisGlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAla 174

DB 63 CAACTGTTGCTATTGACATGACAGACCAAGATGCAATTATTCTCTCTCCAGGCG 122

QY 175 CysArgAsnAspProPheThrGluGluMetThrAlaMetAsnLeuAspArgLysThr 194

DB 123 TGCCGCAACGAATCATTCACCGAGGAGAAATCTCGGCCATGAACCTCGATCGCAGACG 182

QY 195 IleValProTyrLeuGluAsnTyrThrIleGlyProGluValAspHisGlnIleValLys 214

DB 183 GTAGTCCCTCTCTCTTGAAGAACTACAAAGTTGGTCTGTAGCTAGACCCAGATCGCAAA 242

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QY 215 AlaAspValalaGlyAspAlaValLeuThrProValSerAlaSerTriAlaPhePhe 234
Db 243 CTGGCCCTGGCT--GGCCAGCGCTCCACCGCAGCGCCAGCAAGCTGGGCGTCTTT 299
QY 235 ThrPheSerProlylsAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAla 254
Db 300 TCATTACATCCCAAGGCCCTCTCGAGCTGAAAGACGACGCCACAAAGACTCTTGACGCG 359
QY 255 SerThrLysPheValSerThrAspAspAlaLeuSerAlaPheIleTriLys 271
Db 360 TCGTCCAAAGTTGTGTCACTGATGCTCTTTCGGCGCTTTATCGGCAA 410

RESULT 10
BI201068/c
LOCUS BI201068 448 bp mRNA linear EST 10-JUL-2001
DEFINITION o4c12fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
          library Fusarium sporotrichioides cDNA clone o4c12fs 3', mRNA
          sequence.
ACCESSION BI201068
VERSION BI201068.1 GI:14667040
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
          Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
          Department of Chemistry and Biochemistry
          Advanced Center for Genome Technology, University of Oklahoma
          620 Parrington Oval, Norman, OK 73019, USA
          Tel: 405 325 4912
          Fax: 405 325 7762
          Email: broe@ou.edu
          Contact Dr. Marian Beremand regarding clone availability Included
          is the best homolog from a blastx search of Genbank nr 04-09-01
          694 4e-73 gi|4378882|gb|AAD197 (AF127176)
          trichothecene3-O-acetyltransfer
          Seq primer: M13-20
          High quality sequence stop: 303.
FEATURES
          source
          1..448
             /organism="Fusarium sporotrichioides"
             /mol_type="mRNA"
             /strain="Tri 10"
             /db_xref="taxon:5514"
             /clone="o4c12fs"
             /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
             cDNA library"
             /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
             XhoI; 5' end of cDNA cloned into EcoRI site of
             pBluescript; 3' end of cDNA cloned into XhoI site of
             pBluescript"
ORIGIN
Alignment Scores:
Pred. No.: 2,55e-50 Length: 448
Score: 555.00 Matches: 102
Percent Similarity: 90.23% Conservative: 18
Best Local Similarity: 76.69% Mismatches: 13
Query Match: 23.78% Indels: 0
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI201068 (1-448)

QY 319 IlecGlyLurleAlaAenGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338
Db 447 GTGCCCGAAATCGCCACGAACCACTTGGCGACACAGATCAGCGCTGCCCTCGGAATC 388

```

```

QY 339 AspProLaserMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnPro 358
Db 387 AACAGTGTATCGTTTGGCGAGACGAACAAGCTTTGGCGAGTACATGCGATGGCTGCT 328
QY 359 AspLysSerAenValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSer 378
Db 327 GACAAGTCGACGCTCCCTGACCGCGATCGGAATCCGTCAAGCAGCATCATGCTGAGT 268
QY 379 SerTriAlaLysValGlyLeuTriAspTyrAspPheGlyLeuGlyLeuGlyProGlu 398
Db 267 TCTTGGGCGCAAGTGGGATGCTGGAGATGACATTTGGTTTGGTGGTGAAGCTGAG 208
QY 399 ThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLys 418
Db 207 AGTGTGAGAAGACCTCGCTTTGAACCTTTTGAAGATTTGATGTACTTTATATCCCAAGA 148
QY 419 ProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLys 438
Db 147 CTTGATGGGAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAG 88
QY 439 AlaAspLysGluTriThrLysTyrAlaGlnTyrValGly 451
Db 87 CGCGATGAGGATGGACAAGTACGCAAGTATATTGGG 49

RESULT 11
BI192008
LOCUS BI192008 514 bp mRNA linear EST 10-JUL-2001
DEFINITION l4c09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
          library Fusarium sporotrichioides cDNA clone l4c09fs 5', mRNA
          sequence.
ACCESSION BI192008
VERSION BI192008.1 GI:14665687
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
          Beremand,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
          Department of Chemistry and Biochemistry
          Advanced Center for Genome Technology, University of Oklahoma
          620 Parrington Oval, Norman, OK 73019, USA
          Tel: 405 325 4912
          Fax: 405 325 7762
          Email: broe@ou.edu
          Contact Dr. Marian Beremand regarding clone availability Included
          is the best homolog from a blastx search of Genbank nr 04-09-01
          730 3e-77 gi|4378882|gb|AAD197 (AF127176)
          trichothecene3-O-acetyltransfer
          Seq primer: T3
          High quality sequence stop: 476.
FEATURES
          source
          1..514
             /organism="Fusarium sporotrichioides"
             /mol_type="mRNA"
             /strain="Tri 10"
             /db_xref="taxon:5514"
             /clone="l4c09fs"
             /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
             cDNA library"
             /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
             XhoI; 5' end of cDNA cloned into EcoRI site of
             pBluescript; 3' end of cDNA cloned into XhoI site of
             pBluescript"
ORIGIN
Alignment Scores:
Pred. No.: 1.84e-49 Length: 514
Score: 548.00 Matches: 101

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Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
557 3e-57 gi|4378882|gb|AAD197 (AF127176)  
trichothecene3-O-acetyltransfer  
Seq primer: T3  
High quality sequence stop: 361.

# FEATURES

Location/Qualifiers  
1..392  
/organism="Fusarium sporotrichioides"  
/mol\_type="mRNA"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
cDNA library"  
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBluescript; 3' end of cDNA cloned into XhoI site of  
pBluescript"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,02e-47 Length: 392  
Score: 530.50 Matches: 102  
Percent Similarity: 87.02% Conservative: 12  
Best Local Similarity: 77.86% Mismatches: 16  
Query Match: 22.73% Indels: 1  
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x BI192452 (1-392)

Qy 117 AlaProGlyThrLeuProGlyThrGlyProGlyThrGlyProAspProLysProVal 136  
Db 3 GCTCCGAGGAGACATTAGCTATCGGACCTGGCAATGGCCCCCAACGCCGAGCTGTG 62  
Qy 137 IleLeuLeuGlnLeuAenPheIleLysGlyGlyLeuLeuLeuThrValAenglyGlnHis 156  
Db 63 TTGCTATTGAGCTCACTTCAATTAAGGCGGACTATTCTCACCCTCAACGGACACAT 122  
Qy 157 GlyAlaMetAspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArg 176  
Db 123 GGTGCTATGGACATGACAGGACAGATGCAATTATTCTCTCCAAAGGCGTCCGC 182  
Qy 177 AsnAspProPheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleVal 196  
Db 183 AACGATATTACCGGAGGAGAAATCTCGGCATGAACCTCGATCGCAAGACGGTAGTC 242  
Qy 197 ProTyrLeuGluAenTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAsp 216  
Db 243 CCTCTCTGAAACTACAAAGTTGGTCTGAGCTATACCACCATCGCAACCTGGCG 302  
Qy 217 ValAlaGlyGlyAspAlaValLeuThrProValSerAlaSerTrpAlaPheThrPhe 236  
Db 303 CTCTGCT---GGCGAGCTGCCACCGCCGCGCAAGCAAGCTGGGCGTTCTTTTCATC 359  
Qy 237 SerProLysAlaMetSerGluLeuLysAspAla 247  
Db 360 ACTCCCAAGGCCCTCTCGAGCTGAAAGACGCA 392

RESULT 14  
BI191997  
LOCUS BI191997.1 GI:14665676 518 bp mRNA linear EST 10-JUL-2001  
DEFINITION 14b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA  
library Fusarium sporotrichioides cDNA clone 14b10fs 5', mRNA  
sequence.

ACCESSION BI191997  
VERSION BI191997.1  
KEYWORDS EST.  
SOURCE Fusarium sporotrichioides  
ORGANISM Fusarium sporotrichioides  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
REFERENCE 1 (bases 1 to 518)

# AUTHORS

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,  
Beremand,M. and Roe,B.  
Analysis of a Fusarium sporotrichioides EST database  
Unpublished (2001)  
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
Department of Chemistry and Biochemistry  
Advanced Center for Genome Technology, University of Oklahoma  
620 Parrington Oval, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu

## TITLE

## JOURNAL

## COMMENT

Contact Dr. Marian Beremand regarding clone availability Included  
is the best homolog from a blastx search of Genbank nr 04-09-01  
712 3e-75 gi|4378882|gb|AAD197 (AF127176)  
trichothecene3-O-acetyltransfer

Seq primer: T3

High quality sequence stop: 484.

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Location/Qualifiers  
1..518  
/organism="Fusarium sporotrichioides"  
/mol\_type="mRNA"  
/strain="Tri 10"  
/db\_xref="taxon:5514"  
/clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed  
cDNA library"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; 5' end of cDNA cloned into EcoRI site of  
pBluescript; 3' end of cDNA cloned into XhoI site of  
pBluescript"

## source

## ORIGIN

Alignment Scores:  
Pred. No.: 1,76e-47 Length: 518  
Score: 530.00 Matches: 98  
Percent Similarity: 87.69% Conservative: 16  
Best Local Similarity: 75.38% Mismatches: 16  
Query Match: 22.71% Indels: 0  
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI191997 (1-518)

Qy 2 AlaPheLysIleGleLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21  
Db 127 TCTTTTGACATGAGCTCGACATCATCGCCAGCAACCGCTCTTCTTCAATCTACACC 186  
Qy 22 GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr 41  
Db 187 CAGATCAGTCTCGTTTACCCGCTCTGTATCCCTCCAGTATCCACCATCGTCAGCACC 246  
Qy 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61  
Db 247 CTTGAGGAAGGCTAAACGCTCTCTCAACCTTCCCATGGGTCCGCGCCGAGGTCAAG 306  
Qy 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81  
Db 307 ACCGAGGCATTCAGCGAAGAAACACAGAACTTCCAGATCATTCATATGAGGAGACA 366  
Qy 82 ProArgValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101  
Db 367 CCCCGTCTTGGTGAAGACCTCCGTGATGATTCCTCAGCGCCCAACGATCAGGGGTG 426  
Qy 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121  
Db 427 AGAAGCGCGGTTCCTCCCTTAGAGATGTTGACGAGAACGTGTCGCTCCGAGGAGACA 486  
Qy 122 LeuProIleGlyProGlyThrGlyProAsp 131  
Db 487 TTAGCTATCGGACTGGCAATGGCCCAAC 516

RESULT 15  
BI192498/c  
LOCUS BI192498 423 bp mRNA linear EST 10-JUL-2001

DEFINITION m4f10fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone m4f10fs 3', mRNA sequence.  
 ACCESSION BI192498  
 VERSION BI192498.1 GI:14666177  
 KEYWORDS EST.  
 SOURCE Fusarium sporotrichioides  
 ORGANISM Fusarium sporotrichioides  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.  
 REFERENCE 1 (bases 1 to 423)  
 AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.  
 TITLE Analysis of a Fusarium sporotrichioides EST database  
 JOURNAL Unpublished (2001)  
 COMMENT Other ESTs: m4f10fs.r1  
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broe@ou.edu  
 Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 652 3e-68 gi|4378882|gb|AAD197 (AF127176)  
 trichothecene3-O-acetyltransfer  
 Seq primer: M13-20  
 High quality sequence stop: 290.

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 /clone\_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"

## ORIGIN

Alignment Scores:  
 Pred. No.: 3,55e-47 Length: 423  
 Score: 526.00 Matches: 96  
 Percent Similarity: 91.20% Conservative: 18  
 Best Local Similarity: 76.80% Mismatches: 11  
 Query Match: 22.54% Indels: 0  
 DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x BI192498 (1-423)

QY	327	LeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArgGlnArg	346
DB	423		
QY	347	ThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsnValSerLeuThr	366
DB	363		
QY	367	AlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLysValGlyLeuTrp	386
DB	303		
QY	387	AspTyrAspPheGlyLeuGlyLysProGluThrValArgArgProIlePheGlu	406
DB	243		
QY	407	ProValGluSerLeuMetTyrPheMetProLysLysProAspGlyGluPheCysAlaAla	426
DB	183		

QY	427	LeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLysGluTrpThrLysTyr	446
DB	123		
QY	447	AlaGlnTyrValGly	451
DB	63	GCAGAATATATTGGG	49

Search completed: January 24, 2005, 09:07:35  
 Job time : 4367 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 24, 2005, 05:23:41 ; Search time 126 Seconds

(without alignments)  
2544.173 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 NAFKIQDLTGLGQLGLSIY.....EDMDRLKADKWTQYAVYG 451

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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5: /cgn2\_6/prodata/1/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	1356	3	US-09-538-414-5
2	2334	100.0	1356	4	US-10-074-279-5
3	1860.5	79.7	1403	3	US-09-538-414-1
4	1860.5	79.7	1403	4	US-10-074-279-1
5	1860.5	79.7	12949	3	US-09-538-414-11
6	1860.5	79.7	12949	4	US-10-074-279-11
7	1860.5	79.7	13737	3	US-09-538-414-10
8	1860.5	79.7	13737	4	US-10-074-279-10
9	962.5	41.2	1425	3	US-09-538-414-7
10	962.5	41.2	1425	4	US-10-074-279-7
11	142	6.1	1347	3	US-09-457-046B-55
12	134	5.7	1542	1	US-08-207-904-1

13	134	5.7	3706	1	US-08-207-904-16	Sequence 16, Appl
14	132	5.7	1317	3	US-09-457-046B-27	Sequence 27, Appl
15	113	4.8	1320	3	US-09-457-046B-44	Sequence 44, Appl
16	112	4.8	1326	3	US-09-457-046B-53	Sequence 53, Appl
17	110.5	4.7	5577	4	US-09-489-039A-4209	Sequence 4209, Ap
18	108	4.6	4756	4	US-09-023-655-1461	Sequence 1461, Ap
19	108	4.6	5117	3	US-08-854-585-1	Sequence 1, Appli
20	108	4.6	5117	4	US-09-447-533-1	Sequence 1, Appli
21	108	4.6	5117	5	PCT-US95-05512-1	Sequence 1, Appli
22	106.5	4.6	911	3	US-09-457-046B-19	Sequence 19, Appl
23	106.5	4.6	911	3	US-09-457-046B-21	Sequence 21, Appl
24	105.5	4.5	957	4	US-08-961-527-371	Sequence 371, App
25	105.5	4.5	44377	2	US-08-804-227C-7	Sequence 7, Appli
26	105.5	4.5	44377	2	US-08-804-198-1	Sequence 1, Appli
27	104.5	4.5	2310	4	US-09-248-796A-4162	Sequence 4162, Ap
28	104	4.5	908	3	US-09-457-046B-23	Sequence 23, Appl
29	102.5	4.4	2433	4	US-09-583-110-1691	Sequence 1691, Ap
30	102.5	4.4	8697	4	US-08-961-527-133	Sequence 123, App
31	102	4.4	16836	3	US-09-147-236-1	Sequence 1, Appli
32	102	4.4	16836	3	US-09-147-236-10	Sequence 10, Appl
33	102	4.4	16836	4	US-09-522-474-1	Sequence 1, Appli
34	102	4.4	16836	4	US-09-522-474-10	Sequence 10, Appl
35	101.5	4.3	2388	4	US-09-252-991A-14064	Sequence 14064, A
36	100.5	4.3	5607	4	US-09-614-221A-80	Sequence 80, Appl
37	99.5	4.3	1512	3	US-09-142-514-1	Sequence 1, Appli
38	99.5	4.3	2304	4	US-09-614-221A-178	Sequence 178, App
39	99.5	4.3	8855	2	US-08-542-003-1	Sequence 1, Appli
40	99.5	4.3	8855	2	US-08-322-760A-1	Sequence 1, Appli
41	99.5	4.3	8855	4	US-09-236-949-1	Sequence 1, Appli
42	99.5	4.3	11601	2	US-08-222-617A-3	Sequence 3, Appli
43	99.5	4.3	11601	2	US-08-222-617A-24	Sequence 24, Appl
44	99	4.2	920	3	US-09-457-046B-1	Sequence 1, Appli
45	99	4.2	2208	5	PCT-US93-00031-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-538-414-5  
; Sequence 5, Application US/09538414  
; Patent No. 6346655  
; GENERAL INFORMATION:  
; APPLICANT: Salmeron, J.  
; APPLICANT: Hohn, T.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/09/538,414  
; CURRENT FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-09-538-414-5

Alignment Scores:  
Pred. No.: 1.54e-257 Length: 1356  
Score: 2334.00 Matches: 451  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-614-954-6 (1-451) x US-09-538-414-5 (1-1356)

QY 1 MetAlaPhyLleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20

Db 1 ATGGCTTTCAAGATACAGCTCGACACCCCTGGCCAGCTACAGGCCCTCCTTTTCGATCTAC 60  
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40  
Db 61 ACCCAATCAGTCTCTCTACCCCGTCTGATATCTCTCAATATCCACTATTGTTCAGC 120  
QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal 60  
Db 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTTCGAGGCCAGGTC 180  
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
Db 181 AAAGCCGAGGGCAATTAGCAGGGGAAACACAGGAACCTCTCTTATCGCTCCCTTTTGAGGAC 240  
QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100  
Db 241 GTTCTCGTGTGTAGTGAAGACCTCCCGGATGATCCTTCAGCGCCACGATCGAGGGT 300  
QY 101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120  
Db 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGGCCCAAGGAAG 360  
QY 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln 140  
Db 361 ACCTTACCTATTGGACCTGTGTAATCTGTCGCGACGACCCAAAGCCTGTAATTTCTATTGCGAG 420  
QY 141 LeuAsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
Db 421 CTCACCTTATCAGGGCGGACCTCATCTCTCATCTGTCAAGCAGCAGCAGCTGTATGGAT 480  
QY 161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180  
Db 481 ATGGTAGGCCAAGATCGGTGTATCGCTACTCTCCAAGCGGTGCGTAACGACCCATTC 540  
QY 181 ThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGln 200  
Db 541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTGAA 600  
QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220  
Db 601 AACTATACGATTGGCCCGGAGGTAGATCATCATGATTGTCAAGCTGATGTAGCTGTGTGT 660  
QY 221 AspAlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAla 240  
Db 661 GACGCTGTTCTACCGCGGTCACTGCAAGCGTGGCGGTCTTCTACATTCAGCCCAAGGCC 720  
QY 241 MetSerGluLeuLysAspAlaIleThrLysThrLeuAspAlaSerThrLysPheValSer 260  
Db 721 ATGTCAAGCTCAAGGATGCTGTACCAAGACTCTTGAAGCATCAACAAGTTCTGTGTG 780  
QY 261 ThrAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArg 280  
Db 781 ACTGACGATGCTCTTTTCGGCGTTTCATCTGGAAATCGGCTCTCGCGTGGTCTCGAAGA 840  
QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
Db 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGGCAATGGGT 900  
QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGly 320  
Db 901 GTCTCGAAACAACATCACCGGCTTCTTCAAAACATGACCTTACCAACATCGACCATCGGC 960  
QY 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340  
Db 961 GAAATCGCCACAGGTCACTCGGCGCAACAGCATACGCGCTTCGTTTCAGACTCGACCCC 1020  
QY 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrIleuHisAsnAsnProAspLys 360  
Db 1021 GCAGCATGCGCCAGCGAAACAAGGCTCTCGCAGCGTACCTGCAACAACCCCGACAAG 1080  
QY 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrp 380  
Db 1081 TCCAACGTATCCCTGACGGCTGATCGGAGCCCATCTACCAAGCGTCACTGCTGATCTTGG 1140

QY 381 AlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThrVal 400  
Db 1141 GCCAAGTGGGACTCTGGGATTCAGACTTTGGCTCGGACTGGTAAGCCCGAGACTGTG 1200  
QY 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420  
Db 1201 AGACGCCCAATCTTTGAGCCTGTGAGAGCTTGTATCTTTATGCCCAAGAAGCCTGAT 1260  
QY 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAsp 440  
Db 1261 GCGAGTCTCTGCGCGCGCTTTCTCTGAGGATGAGGATATGACCGATTGAAGGCGGAT 1320  
QY 441 LysGluTrpThrLysTyrAlaGlnTyrValGly 451  
Db 1321 AAGGAGTGACCAAGTATGCGCAGTACGTTGGT 1353

## RESULT 2

US-10-074-279-5  
; Sequence 5, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: Fusarium graminearum  
US-10-074-279-5

Alignment Scores:  
Pred. No.: 1,54e-257 Length: 1356  
Score: 2334.00 Matches: 451  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-614-954-6 (1-451) x US-10-074-279-5 (1-1356)

QY 1 MetAlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyr 20  
Db 1 ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGTACACGAGCCCTCCTTTTCGATCTAC 60  
QY 21 ThrGlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSer 40  
Db 61 ACCCAATCAGTCTCTCTTACCCCGTCTGATTTCTCTCAATATCCCACTATTGTTCAGC 120  
QY 41 ThrPheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnVal 60  
Db 121 ACCTTCGAGCAAGGTCTTAAAGCGCTTCTCGAAGCGCTCCCATGGGTTCGAGGCCAGGTC 180  
QY 61 LysAlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAsp 80  
Db 181 AAAGCCGAGGGCAATTAGCAGGGGAAACACAGGAACCTCTCTTATCGCTCCCTTTTGAGGAC 240  
QY 81 ValProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGly 100  
Db 241 GTTCTCGTGTGTAGTGAAGACCTCCCGGATGATCTCTTACGCGCCACGATCGAGGGT 300

101 MetArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLys 120  
 Db ATGAGAAAGCGGATACCTATGGCGATGTTTACGAGAACATCATCGGCCAAGGAAG 360  
 121 ThrLeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGln 140  
 Db ACCTTACCTATTGGACCTGGTACTGCTCCGACGACCCAAAGCCTGTAATTTCTATTGGAG 420  
 141 LeuAsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAsp 160  
 Db CTCAACTTCATCAAGGCGGACTCATCTCACTGTCAACGGACAGCACGGTGTATGGAT 480  
 161 MetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPhe 180  
 Db ATGGTAGGCAAGATCGGTGATCCGTCTACTCTCCAAAGCGGTGCGTAACGACCCATTTC 540  
 181 ThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGlu 200  
 Db ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATGTTCTTACCTTGA 600  
 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220  
 Db AACTATACGATTGGCCCGCGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGGTGT 660  
 221 AspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAla 240  
 Db GACGCTGTCTTCACGCGCGGTCACTGCAAGCTGGCGCTTCTTCAATTCAGCCCCAAGGCC 720  
 241 MetSerGluLeuLysAspAlaThrLysThrLeuAspAlaSerThrLysPheValSer 260  
 Db ATGTCAAGCTCAAGGATGCTGTACCAAGACTCTTGACGATCAACAAGTTCTGGTGTG 780  
 261 ThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArg 280  
 Db ACTGACGATGCTCTTTCGGGGTTCATCTGGAATCGGCTCTCGCGTGGCTCGAAGA 840  
 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
 Db ATCGATGGCTCTGCACCTACCGAGTCTGCGGTGCTGTGATCTCGACCGGCAATGGGT 900  
 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisSerThrIleGly 320  
 Db GTCTCGAAACAACCTACCGAGCCTTCTTCAAAACATGACCTTACCACAACTCGACCATCGGC 960  
 321 GluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspPro 340  
 Db GAATTCGCCAACGACCTCACTCGGCGCAACAGCATACGCTTCTGTTCAAGACTCGACCCC 1020  
 341 AlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLys 360  
 Db GCGAGCATGCGCCAGCGCAACAGAGGTCTCGGACGTACTCGACCAACAACCCCGACAAG 1080  
 361 SerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyr 380  
 Db TCCAACGTATCTCTGACGCTGATGGGACCCATCTACCAAGCTCATGCTGAGTTCTTGG 1140  
 381 AlaLysValGlyLeuTyrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400  
 Db GCCAAGTGGGACTCTGGGATACGACTTGGCTCGGACTGGGTGAAGCCCGAGACTGTG 1200  
 401 ArgArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAsp 420  
 Db AGACGCCCAATCTTTGAGCTGTTGAGAGCTTGTATGTTATGCCAAGAGCCCTGAT 1260  
 421 GlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLysAlaAsp 440  
 Db GGGGAGTCTTCTGCGCGCTTCTCTGAGGATGAGGATATGACCGGATTTGAAGGCGGAT 1320  
 441 LysGluTyrThrLysTyrAlaGlnTyrValGly 451  
 Db AAGGATGGACCAAGTATGCGCAGTACGTTGGT 1353

RESULT 3

US-09-538-414-1  
 ; Sequence 1, Application US/09538414  
 ; Patent No. 6346655  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hohn, T.  
 ; APPLICANT: Salmeron, J.  
 ; APPLICANT: Peters, C.  
 ; APPLICANT: Kendra, D.  
 ; APPLICANT: Reinders, J.  
 ; APPLICANT: Kuznia, R.  
 ; APPLICANT: Dill-Mackey, R.  
 ; TITLE OF INVENTION: Transgenic Plant and Methods  
 ; FILE REFERENCE: sequencelist  
 ; CURRENT APPLICATION NUMBER: US/09/538,414  
 ; CURRENT FILING DATE: 2000-03-29  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1403  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium sporotrichioides  
 US-09-538-414-1

## Alignment Scores:

Pred. No.: 3,18e-203 Length: 1403  
 Score: 1860.50 Matches: 349  
 Percent Similarity: 88.67% Conservative: 50  
 Best Local Similarity: 77.56% Mismatches: 50  
 Query Match: 79.71% Indels: 1  
 DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x US-09-538-414-1 (1-1403)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21  
 Db TCTTTTGACATAGAGCTCGACATCATCGCCAGCAACCCGCTCTTCTTCAATCTACACC 96  
 QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41  
 Db CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 156  
 QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61  
 Db CTTGAGGAGGCGCTAAACGCTCTCTCAAACTTCCCATGGGTCCGGCCAGGTCAAG 216  
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81  
 Db ACCGAGGGGATCAGCGAAGAAACACAGAACTTCCAAGTCAATCATATGAGGAGACA 276  
 QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101  
 Db CCGCGTCTGTGTGTAAGACCTCCGTGATGATTCCTCAGCGCCAAACGATCGAGGGGTG 336  
 QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121  
 Db AGAAAGCGGGTTCCTCCCTTAGAGATGTTTGAAGAACGTGCTGCTCCGAGGAAGACA 396  
 QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141  
 Db TTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCCTGTGTTGTTATGAGCTC 456  
 QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161  
 Db AACTTCATTAAAGGCGGACTCATCTCAGCTCAACGGCAACATGCTGTATGGACATG 516  
 QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181  
 Db ACAGGCAAGATGCAATATTATGCTTCTCTCAAGCGTGGCGCAACCAATCATTCACC 576  
 QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201  
 Db GAGGAGGAATCTCGGCCCATGAACCTCGATCGCAGACCGGTAGTCTCTCTCTTGAANAC 636



Db 874 GATGCTTCCACACTACTGAATCTCGCGGCTGTGACATGTCGGGGCCCAATGGCGTA 933  
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321  
Db 934 TCAAGCACATACCCAGGCTTCTTCAAAACATGACCTACCATGACTCGACCGTGGCGAA 993  
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341  
Db 994 ATCGCAACGAACCACTTGGCGCAACAGCATCAAGCTCGCTCGGAACTCAACAGTGAT 1053  
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnProAspLysSer 361  
Db 1054 CGTTTCGGACGACGAACACAGCTTTGGCGACGTATCATGATGGCTGCTGACAAAGTCG 1113  
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381  
Db 1114 AGCGTCTCCTGACCGCGCATCGAATCCGTCAAGCAGCATCATGCTGAGTCTCTGGCC 1173  
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401  
Db 1174 AAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGTAAGCTCGAGAGTGTGAGA 1233  
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421  
Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGTACTTTATGCCCCAAGACCTGATGG 1293  
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441  
Db 1294 GAGTTTACGGCGTCCATTTCTTGAGGGATGAGGATATGAGAGACTAAAGCGGATGAG 1353  
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451  
Db 1354 GAGTGACAAAGTACGCAAGTATATTTGGG 1383

## RESULT 5

US-09-538-414-11

; Sequence 11, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/09/538,414

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 12949

; TYPE: DNA

; ORGANISM: Plasmid

US-09-538-414-11

## Alignment Scores:

Pred. No.:	1,22e-201	Length:	12949
Score:	1860.50	Matches:	349
Percent Similarity:	88.67%	Conservative:	50
Best Local Similarity:	77.56%	Mismatches:	50
Query Match:	79.71%	Indels:	1
DB:	3	Gaps:	1

US-10-614-954-6 (1-451) x US-09-538-414-11 (1-12949)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21  
Db 11282 TCTTTTACATAGAGTCGACATCATCGGCGCAACCCGCTCTCTTCAATCTACACC 11341  
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41

Db 11342 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCCATATCCCACTATGTCACACC 11401  
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61  
Db 11402 CTTGAGGAGGCTTAAACGCCTCTCTCAACCTTCCCATCGGTCGCGGCCAGGTCAG 11461  
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81  
Db 11462 ACCGAGGGCATCAGCGAAGAAACACAGAACTTCCAAATCATTCATATGAGGACA 11521  
QY 82 ProArgValValValIleAspLeuArgAspProSerAlaProThrIleGluGlyMet 101  
Db 11522 CCCGCTGTGTGTAAGACCTTCGTGATGATTCCTAGCGCAACGATCAGAGGGTTG 11581  
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121  
Db 11582 AGAAGGCGGGTTTCCCTTAGAGATGTTTGACGAGAACGTGCTCGGAGGAGACA 11641  
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141  
Db 11642 TTAGCTATCGGACCTGGCAATGCCCAACGACCCGAAAGCTGTGTGCTATTGCGACTC 11701  
QY 142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161  
Db 11702 AACTTCATTAAAGGCGGACTCATTCACCGTCAACGCAACATGCTGCTATGGACATG 11761  
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181  
Db 11762 ACAGGACAGATGCAATTTATGCTTCTCCNAGCGTGGCGCAACGAACTATTCACC 11821  
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201  
Db 11822 GAGGAGGAAATCTCGGCCATGAACCTCGATCGCAGACGCTAGTCCCTCTCTTGA AAC 11881  
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221  
Db 11882 TACAAAGTTGGTCTGAGCTAGCACCAACAGATCGCCAAACCTGCGCGCTGCT---GGCGAC 11938  
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241  
Db 11939 GTTCACCCGCGACCGGCAAGGCAAGCTGGGGTCTTTTTCATCTCACTCCCAAGGCGCTC 11998  
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261  
Db 11999 TCGGAGCTGAAAGCGCAGCCACAAAGACTCTTGACGCGTCTGTCCAAGTTTGTCAACT 12058  
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281  
Db 12059 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGTCTCGCAAGATTG 12118  
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301  
Db 12119 GATGCTTCACACCTACTGAATTTCTCCGCGCTGTGACATGTCGGGGGCCCAATGGCGTA 12178  
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321  
Db 12179 TCAGCACATACCCAGGCTTCTTCAAAACATGACCTACCATGACTCGACCGTGGCGAA 12238  
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341  
Db 12239 ATCGCAACGAACCACTTGGCGCAACAGCATCACGCTCGCTCGGAACTCAACAGTGAT 12298  
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361  
Db 12299 CGTTTGGCAGAGCAACCAAGCTTTGGCGAGCATCATGATGGCTGCTGCAAGTCG 12358  
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381  
Db 12359 AGCGTCTCCTGACCGCGCATGCGAATCCGTCAAGCAGCATCATGCTGAGTCTCTGGGCC 12418  
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401

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Db 12419 AAGTGGGATCTGGGAGTATGACTTTGGGTTGGACTGGTAAGCCTGAGAGTGTGAGA 12478
Qy 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 12479 AGACCTCGCTTGAACCTTTGAGAGTTGATGACTTTATGCCCAAGAGCCTGATGG 12538
Qy 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 12539 GAGTTTACGGCGTCCATTTCTCTGAGGATGAGATATGAGAGACTAAAGCGGATGAG 12598
Qy 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 12599 GAGTGGACAAAGTACGCAAGTATATTTGGG 12628

RESULT 6
US-10-074-279-11
; Sequence 11, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Alignment Scores:
Pred. No.: 1,22e-201 Length: 12949
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 4 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-11 (1-12949)
Qy 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 11282 TCTTTTGACATAGAGCTCGACATCATCGCGCAGCAACCGCTTCTTCAATCATACACC 11341
Qy 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 11342 CAGATCAGTCTCGTTTACCGCTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 11401
Qy 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 11402 CTTGAGGAAGGCTTAAAGCCCTCTCTCAACCTTCCCATGGGTGCGGGCGAGGTCAAG 11461
Qy 62 AlaGluGlyIleSerGluGlyAenThrGlyThrSerPheIleValProPheGluAspVal 81
Db 11462 ACCGAGGGCATCAGCGAGGAACACAGGACTTCCAAAGTCAATTCATATGAGGAGACA 11521
Qy 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db 11522 CCCCGTCTGTGTGTAAGACCTCCGTGATGATTCTCCAGCGCAACCATCGAGGGGTG 11581
Qy 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 11582 AGAAAGCGCGGTTTCCCTTTAGAGATGTTTGGACGAGAACGTGCTCGCTCCGAGGAAGACA 11641
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## RESULT 7

US-09-538-414-10

; Sequence 10, Application US/09538414

; Patent No. 6346655



```
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerton, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; US-09-538-414-10

Alignment Scores:
Pred. No.: 1 34e-201 Length: 13737
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 3 Gaps: 1

US-10-614-954-6 (1-451) x US-09-538-414-10 (1-13737)
QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleThr 21
DB 51 TCTTTTGACATAGAGCTCGACATCATCGCCAGCAACCGCTCTCTTCAATCTACACC 110
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr 41
DB 111 CAGATCAGTCTCTGTACCCGCTCTGTATCCCTCCAGTATCCACCATCGTCAGCACC 170
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61
DB 171 CTTGAGGAAGGCTTAAAGCCCTCTCAAAACCTTCCCATGGTCCGGCCAGGTCAG 230
QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProGluAspVal 81
DB 231 ACCGAGGCGCATCGCAGGAGAACACAGGAACCTTCCCAAGATCATTCATGAGGAGACA 290
QY 82 ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
DB 291 CCCCGTCTTGTGTGAAGACCTCCGTCATGATTCTCAGCGCCACGATCGAGGGGTG 350
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
DB 351 AGAAAGCGGGTTCCTCCCTTAGAGATGTTTGAGGAGAACGTCGCTCCGAGGAAGACA 410
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
DB 411 TTAGCTATCGGACTCGCAATGSCCCCAAGACCCGAGCGCTGTGTCTATTGACAGCTC 470
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
DB 471 AACTTCATTAAAGGCGGACTCATCTCACCCTCAAGCGCAACATGGTGTATGACATG 530
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
DB 531 ACAGGACAGATCAATATTCTCTCTCTCAAGCGCGGCGCAACGAATCATTCACC 590
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
DB 591 GAGGAGGAATCTCGGCGCATGAACCTCGATCGGACAGCGTAGTCTCTCTCTTGAAC 650
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyAsp 221
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DB 651 TACAAAGTTGGTCTGAGCTAGACACCAAGATCGCCAAACCTCGCGCTGCT---GGCGAC 707
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
DB 708 GTCCACCCGACCGCCCAAGGCAAGCTGGCGGTCTTTTCATTCACTCCCAAGGCCCTC 767
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
DB 768 TCGGAGCTGAAGAGCGCAGCCCAAGACTCTTGACGCGCTCGTCCCAAGTTGTGTCAACT 827
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
DB 828 GATGATGCTCTTTTCGCGGTATTCTGGCAATCAACCTCGCGGTAGCTCTCGCAAGATTG 887
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAlaAspAlaArgProAlaMetGlyVal 301
DB 888 GATGCTTCACACCTACTGAATTCGCGCGCTGTGCACATCGCGGGCCCAATGGCGGTA 947
QY 302 SerAsnAsnTyrProGlyLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
DB 948 TCAAGCACATACCCAGGCTCTCTCAAAACATGACCTACATGACCTCGACCGCTCGCGGAA 1007
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
DB 1008 ATCGCCCAACGAACCTTGGCGCAACAGCATCACGCTCGCTCGGAATCTCAACAGTGAT 1067
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
DB 1068 CGTTTGGCGAGCAACACAGCTTTGGCGAGTATCATGTCATCGCTCGCTCGCAAGTCG 1127
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
DB 1128 AGCGTCTCCCTGACCGCGATCGAATCGTCAAGCAGCATCATGTGAGTTCTCTGGGCC 1187
QY 382 LysValGlyLeuTrpAspThrAspPheGlyLeuGlyLysProGluThrValArg 401
DB 1188 AAGGTGGGATGCTGGGAGTATGACTTTGGGTGGACTGGTAAGCCTGAGAGTGTGAGA 1247
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
DB 1248 AGACCTCGCTTTGACCTTTTGAGAGTTTGATGTACTTTATGCCCAAGAGCTGTATGG 1307
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
DB 1308 GAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGAG 1367
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
DB 1368 GAGTGACAAGTACGCAAAAGTATATTGGG 1397
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## RESULT 8

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US-10-074-279-10
; Sequence 10, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerton, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; CURRENT APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
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; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

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Alignment Scores:		
Pred. No.:	1,348-201	Length:
Score:	1860.50	Matches:
Percent Similarity:	88.67%	Conservative:
Best Local Similarity:	77.56%	Mismatches:
Query Match:	79.71%	Indels:
DB:	4	Gaps:
		13737

US-10-614-954-6 (1-451) x US-10-074-279-10 (1-13737)

Qy	2	AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr	21
Db	51	TCCTTTGACATAGACATCGACATCATCGGCAGAACCGCTCTCTTTTCAATCTACACC	110
Qy	22	GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr	41
Db	111	CAGATCAGTCTCGTTTACCCGTCCTGATCCTCCAGCATGCCACCATCTGCACACC	170
Qy	42	PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys	61
Db	171	CTTGAGGAAGGCCTAAACGCCTCTCTCAAAACCTTCCTCATGGTGGCGGCGCAGGTCAAG	230
Qy	62	AlaGluGlyIleSerGlnGlyAsnThrGlyThrSerPheIleValProPheGluAspVal	81
Db	231	ACCGAGGGCATCAGCGAAGGAACAACAGGAATCTCCAGATCATTTCCATATGAGGAGACA	290
Qy	82	ProArgValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet	101
Db	291	CCCCGTCTGTGTGAAGACCTCGTGTATGATTCCTCAGCGCAACGATCGAGGGGTG	350
Qy	102	ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr	121
Db	351	AGAAAGCGGGTTTCCCTTAGAGATGTTTACAGAACGCTCGTCGCTCCGAGGAAAGACA	410
Qy	122	LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu	141
Db	411	TTAGCTATCGGACCTGGCNAATGGCCCCAGACCGAAGACCTGTGTGTCTATTGCGAGCTC	470
Qy	142	AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet	161
Db	471	AACTTCATTAAAGGGCGGACTCATTTCTCACCCTCAACGGCAACAATGCTGTATGGACATG	530
Qy	162	ValGlyClnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr	181
Db	531	ACAGGACAAGATGCAATTATTTCGTTCTCTCCAAGGCGTGGCCACCAAGAAATCATTCACC	590
Qy	182	GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn	201
Db	591	GAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGGGTAGTCCCTCTCTCTTGAAGAAC	650
Qy	202	TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp	221
Db	651	TACAAAGTTGGTCTCGAGCTAGACACACAGATCGCAAAACCTGGCGCCTGTCT--GGCGAC	707
Qy	222	AlaValLeuThrProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMet	241
Db	708	GCTCCACCCGCGACCGGCCAAGCGAAGCTGGGGTCTTTTCATTACATCTCCALAGGCCCTC	767
Qy	242	SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr	261
Db	768	TCGGAGCTGAAGAGACGACCCACAAGAATCTCTTGACGGCTCGTCCAAAGTTTGTCAACT	827
Qy	262	AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle	281
Db	828	GATGATGTCTCTTCGGCGGTTTATCTGGCAATCAACCTCGCGCGTACGTCTCGCAAGATTG	887
Qy	282	AspGlySerAlaProThrGluPheCysArgAlaValAspAlaValAspProAlaMetGlyVal	301

888	DB	GATGCTTCACACCTACTGAAATTTCTCCGCGCTGTGACATGCGGGGCCCAATGGGCGTA	947
302	QY	SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu	321
948	DB	TCAAGCACATACCCAGGCGCTTCTTCAAAACATGACCTACCATCGCTCGACCGTCCGCCAA	1007
322	QY	IleAlaAsnGlnSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla	341
1008	DB	ATGCCCAACGACCCTTTGGCGCAACAGCATCACGCTGCGCTCGGAATCAACAGTGAT	1067
342	QY	SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer	361
1068	DB	TTGCGGAGACGAAACACAGCTTTTGGCGCGCTCATGCTAGCTGCGCTGACAGTCG	1127
362	QY	AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla	381
1128	DB	AGCGTCTCCCTGACCGCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTTCCTGGGCC	1187
382	QY	LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg	401
1188	DB	AAGGTGGGATGCTGGGAGATGATCTTTGGGTTTGGACTGGGTAAAGCTGAGAGTGTGAGA	1247
402	QY	ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly	421
1248	DB	AGACCTCGCTTTGAACCTTTTGGAGATTGTGATCTATTATGCCCCAAGACCTGATGGG	1307
422	QY	GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys	441
1308	DB	GAGTTTACGGCGTCCCAATTTCTTGGAGGGATGAGGATATGGAGAGACTAAAGGCGGATGAG	1367
442	QY	GluTrpThrLysTyrAlaGlnTyrValGly	451
1368	DB	GAGTGCACAAAGTACGCAAGTATATGGG	1397

## RESULT 9

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US-09-538-414-7
; Sequence 7, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Reznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/539,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-7

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Alignment Scores:		
Pred. No.:	3e-100	Length: 1425
Score:	962.50	Matches: 202
Percent Similarity:	62.86%	Conservative: 84
Best Local Similarity:	44.40%	Mismatches: 158
Query Match:	41.24%	Indels: 11
DB:	3	Gaps: 8

US-10-614-954-6 (1-451) X US-09-538-414-7 (1-1425)

Qy	6 GlnLeuAspThrIleuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu 25 
Dp	64 CAACCTGGATATTTGGGCAACAACCTTCGCTATACAACTATACACTCAATATGCTCT 123 ::

QY 26 LeuTyrProValSerSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45  
Db 124 ATCTCGTGTACAGATCTCTTGTCTATGACCATATCTGAATACCTTTAAACAAGAGGA 183  
QY 46 LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 65  
Db 184 CTTGAACATTTGGCTAAATTTCCAGTGGCTAGCAGGAATGCTGTAATGAAGTGCT 243  
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 85  
Db 244 GACGAAGGTAAACCTGCTACAGAAATGTCCTGCGTACAGCAAAATTTCCA---CTTATC 300  
QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105  
Db 301 GTCCAAAGATCTTCGAGAAGATCTGTCGCCCAACAATGGAATTCGCTTGAATAAGCTGAC 360  
QY 106 TyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu---ProIle 124  
Db 361 TTTCTTATCTACATGTTAGACGAAGAAGACTTTTGGCGCTTGGCATGACTATCAATCCACCT 420  
QY 125 GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe 143  
Db 421 GGAACACACTATGATGGCGCCAGAGTGGCGCTGTATTTGCAGTTCAGCAAACTTT 480  
QY 144 IleLysGlyGlyLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly 163  
Db 481 ATCTCGCGCGCTCTTAACTATTTGTCGCGAGCACAATATTATGGATTAACAGGA 540  
QY 164 GlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPheThrGluGlu 183  
Db 541 CAGAAAGTATCATCACTTGTCTCAATTAATCTTGGCACCMAAACTTTCTCTGATGA 600  
QY 184 GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThr 203  
Db 601 GAACCTGCTCTGGAATATAGATAAAGCAAACTTATCTCTTTGTGATGAA---ACT 657  
QY 204 IleGlyProGluValAsp-----HisGlnIleValLysAla-----AspValAlaGly 219  
Db 658 TGGGAACCCGACACCAACGCTAGTTCTATGAATATAGTGGNAACCTCTAGAAATACAAGTGA 717  
QY 220 GlyAspAlaValLeuThrProValSer---AlaSerTyrAlaPhePheThrPheSerPro 238  
Db 718 GAGAAAGGAAGAACAGTCTTGTCTTGGAACTTACTTGGCGCTTATGTAATTTCTGCT 777  
QY 239 LysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe 258  
Db 778 ATCTCATGTCAGATCTGAGGATTTTGGCAATGCAGACATGTACTCTGCGACAAATTT 837  
QY 259 ValSerThrAspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeu 278  
Db 838 GTCTCCACTGATGATATCGTCACTGCTTTCATCTGGAATTCAGTTTCTCGAGCCCTTTA 897  
QY 279 GluArgIleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAla 298  
Db 898 TCTCGACTTAAACCCAGAAACGAATCAAAATTTAGGCGGTCTGTGATGTTAGAAACGG 957  
QY 299 MetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThr 318  
Db 958 CTAGGACTCCCCAAACGATATCAGGGTATTATGTCACATGACCTTTAATACAGGTTC 1017  
QY 319 IleGlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeu 338  
Db 1018 CTGAAAGCTTGGATCATAAAGTTTGGCGCTTCTTGATCATCAGATTCGACGAAGCTA 1077  
QY 339 AspProAla-----SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsn 356  
Db 1078 GACCCCTAAAGTCTTCGATTTGGCGCTATAATACATGCGCACTTCTGCTACGCTCTTACCGCA 1137  
QY 357 AsnProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMet 376  
Db 1138 TGCCCGGACAGACTAAGGTTTCTATACCTCAACCAATTGATTAATCTTGAATATG 1197  
QY 377 LeuSerSerTrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLys 396

Db 1198 GTCAAGTTCGTGGCAAAAGTCAAGCTGTATGAGTTGATTTCATCTAGGCTTGGGAAG 1257  
QY 397 ProGluThrValArgArgProIlePheGluProValGluSerLeuMetTyrPheMetPro 416  
Db 1258 CCCNAGAGTGTACGAGCGCGCGCTTCATTTCCCTTGAGAGCTATATATTTATGCCT 1317  
QY 417 LysLysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArg 436  
Db 1318 AGATCTCCAGAGGTGAATGGTGGTGTCTTTTGCCTTAGAGATAAGATTGGAGTGC 1377  
QY 437 LeuLysAlaAspLysGluTrpThrLysTyrAlaGlnTyrValGly 451  
Db 1378 CTGAATGCGGATAAAGAATGGCAAAATTATGCTACATATAGGA 1422  
RESULT 10  
US-10-074-279-7  
; Sequence 7, Application US/10074279  
; Patent No. 6646184  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1425  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-10-074-279-7  
Alignment Scores:  
Pred. No.: 38-100 Length: 1425  
Score: 962.50 Matches: 202  
Percent Similarity: 62.86% Conservative: 84  
Best Local Similarity: 44.40% Mismatches: 158  
Query Match: 41.24% Indels: 11  
Db: 4 Gaps: 8  
US-10-614-954-6 (1-451) x US-10-074-279-7 (1-1425)  
QY 6 GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu 25  
Db 64 CAATTTGATATTTTGGGACACAACTTCGCTATACAACTATACACTCAATATGCTCT 123  
QY 26 LeuTyrProValSerSerSerGlnTyrProThrIleValSerThrPheGluGlnGly 45  
Db 124 ATCTACCGTGTACAGATCTCTTGTCTCATGACCATATCGTAATACCTTAAACAAGAGGA 183  
QY 46 LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 65  
Db 184 CTTGAACATTTGGCTAAATTTCCAGTGGCTAGCAGGAATGCTGTAATGAAGTGCT 243  
QY 66 SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 85  
Db 244 GACGAAGGTAAACCTGCTAGTACCTACAGAAATGTCCTGACAGCAAAATTTCCA---CTTATC 300  
QY 86 ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly 105  
Db 301 GTCCAAAGATCTTCGAGAAGATCTGTCGCCCAACAATGGAATTCGCTTGAATAAGCTGAC 360  
QY 106 TyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeu---ProIle 124  
Db 361 TTTCTTATCTACATGTTAGACGAAGAAGACTTTTGGCGCTTGGCATGACTATCAATCCACCT 420



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QY 234 PheThrPheSerProLysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAsp 253
DB 706 TTTTACTATAAACTCAGAGATAATAATATCATCAAAACAATGT-----GTTATAGAA 756
QY 254 AlaSerThrLysPheValSerThrAspAlaLeuSerAlaPheIleThrLysSerAla 273
DB 757 GAATGTAAACAATAATTTCTCTGCATTTGAATGTTGTAGTACATAACTTGG-----ATA 810
QY 274 SerArgValArgLeuGluArgIleAspGlySerAlaProThrGluPheCysArgAlaVal 293
DB 811 GCAAGGACAAAGGCTTTTCAAATTCACATAATGAGAAATGTGATGATGCTCTTTTGAATG 870
QY 294 AspAlaArgProAlaMetGlyValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThr 313
DB 871 GACGCGAGGAAATPATTTTAAT-----CCCCCACTTCCAAAGGGA----- 909
QY 314 TyrHisAsnSerThrIleGly-----GluIleAlaAsn 324
DB 910 TATATGTTAATGCCATTTGGTACTTTCATGTGTAAATGAAATGTACAAGACCTCTTAAT 969
QY 325 GluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMetArg 344
DB 970 GGAATCTCTTCGGGCTGTGTAATGATTACAAAGAAATCAAAGATCCCTTTAATTGAGAAT 1029
QY 345 GlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSerAsnValSer 364
DB 1030 TTAAGGTCAGAAATTTGGCG-----AACCAATCTGGAGTAGAT 1068
QY 365 LeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAlaLysValGly 384
DB 1069 -----GAGGAATAATGAAGCATGAAACGTAGTTGGATTGGAGATTGGAGCGGATGGGA 1122
QY 385 LeuTrpAspTyrAspPheGlyLeuGly 393
DB 1123 TTTATGAAGTGGACTTCGGATCGGA 1149

RESULT 12
US-08-207-904-1
; Sequence 1, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; TITLE OF INVENTION: Crossland, Lyle D.
; TITLE OF INVENTION: Another-Specific cDNA Sequences, Genomic
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/207,904
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; INDIVIDUAL ISOLATE: Ant32
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..1412
; US-08-207-904-1

Alignment Scores:
Pred. No.: 3,37e-05 Length: 1542
Score: 134.00 Matches: 104
Percent Similarity: 33.82% Conservative: 58
Best Local Similarity: 21.71% Mismatches: 183
Query Match: 5.74% Indels: 134
DB: 1 Gaps: 24

US-10-614-954-6 (1-451) x US-08-207-904-1 (1-1542)
QY 21 ThrGlnIleSerLeuLeuTyr-----ProValSerAsp 31
DB 165 ACTCATGTACCAACCATTTATTACTACAGGTTTGGCATGATTGTCTTCCATCAACAGAC 224
QY 32 SerSerGlnTyrProThrIleValSerThrPheGluGlnGlyLeuLysArg----- 48
DB 225 AAT-----ATCATCAAAACCCTCAGGACCTCCTAAGCAAGCATTAGTA 269
QY 49 -----PheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGly 64
DB 270 CACTTCTATCCATTGTCTGGTGTTCGATGATGATCGCTGG-----TCC 314
QY 65 IleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgVal 84
DB 315 CGCCTCGAGCTCGACTGTAATGCTCGGAATCGTGTCTCATGCAAGCTGAAACCGAAGCC 374
QY 85 ValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMetArgLysAla 104
DB 375 AAACATAGATGATCTTGGCGATTCTCGCATCCCT----- 410
QY 105 GlyTyrProMetAlaMetPheAspGluAsnIleAlaProArg-----LysThrLeu 122
DB 411 -----GACTTGAACAGCTTGTTCCTCCCGTGTAGACTACACATC 449
QY 123 ProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu--- 141
DB 450 CCAAT-----GATGAATCCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 488
QY 142 AsnPheIleLysGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
DB 489 AAGTTTCAGTGTGTGTGTTGCTCTGAGTTTGCATATATCATCATCTCTGTAGTTGAT--- 545
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAla-----CysArgAsnAspPro 179
DB 546 ---GGCCAAAGTCTCTTTACTTCTCCACCGAATGGGCTAGCCTTCTCGCGAGAGCCCA 602
QY 180 PheThrGluGluGluMetThrAlaMetAsnLeuAspArgLysThrIle----- 195
DB 603 TTAGGGAACGAACCTTTTTCAT-----GATCGAAATTCCTCCGAGCAGGGGAA 650
QY 196 -----ValProTyrLeuGluAsnTyrThrIleGlyProGluValAspHisGln 211
DB 651 CTTCCAAATGTCATATCCAAAGTTTGAGCATTTACAGTTTAAATCCA----- 695
QY 212 IleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrProValSerAlaSerTrp 231
DB 696 -----CCACCACCTTTTGTCTTGAGCAGTCCAGCAGT--- 725
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Db 655 CCTCAATTGTTGAGAAAATTGTTCAA----- 681
Qy 226 ProValSerAlaSerTrpAlaPheThrPheSerProlyseAlaMetSerGluLeuLys 245
Db 682 -----ACATATTTTATATAGATTTTGAGACCAATAAATATATACAA 723
Qy 246 AspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAlaLeu 265
Db 724 CAATCT-----GTTATGGAAGAAGATGAAGAATTTTGCTCTCAITTCGAAGTTGCA 774
Qy 266 SerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAla 285
Db 775 TCAGCACTGACTGG-----ATAGCAAGGACAGAGACTTTTCAAAATTCAGAAAGTGA 828
Qy 286 ProThrGluPheCysArgAlaValAspAlaAArgProAlaMetGlyValSerAsnAsnTyr 305
Db 829 TAGCTGAAAATCTCTTCGGAATGGACATGAGG-----NACTCATTT 870
Qy 306 ProGlyLeuLeuGlnAsnMetThrTyrHisAsnSer-----ThrIleGlyGluIleAla 323
Db 871 AATCCCCCTCTTCCAAGCGGATACTATGGTAACCTCGTATGTTGGTACCGCATGTGCAGTGGAT 930
Qy 324 AsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSer-----GluLeuAsp 339
Db 931 AATGTTCAAGACCTCTTAAGTGGATCTCTTTGCGTACTAATGATTAATAAGAAATCA 990
Qy 340 ProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAsp 359
Db 991 AAGGTCCTTTAAATCAATATTCAGTCAAGAGCTGTGGTG-----AAGCCATCT 1041
Qy 360 LysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSer 379
Db 1042 GAATTGGATGTGAATGAATCAATGAA-----AACGTAGTTGCAATTTGCTGAT 1089
Qy 380 TrpAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLysProGluThr 399
Db 1090 TGGAGCCGATGGGATTTGATGAAGTGGATTTGGTGGGGAATCGGTGAGTGTAAAG 1149
Qy 400 ValArgArgProIlePheGluProValGluSerLeuMet-----TyrPheMet----- 415
Db 1150 -----CCTGTGCACACACAGTCTGCGTAGCAATGCAAAATTTTCTTTTCCTA 1200
Qy 416 -----ProLysLysProAspGly 421
Db 1201 AAACCTTCCAAGAACCAAGCCCGATGA 1227

RESULT 15
US-09-457-046B-44
; Sequence 44, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-457-046B-44

Alignment Scores:
Pred. No.: 0.00667 Length: 1320
Score: 113.00 Matches: 93
Percent Similarity: 35.84% Conservative: 69
Best Local Similarity: 20.58% Mismatches: 186
Query Match: 4.84% Indels: 104
DB: 3 Gaps: 20

US-10-614-954-6 (1-451) x US-09-457-046B-44 (1-1320)
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Qy 5 IleGlnLeuAspThrIleuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSer 24
Db 82 CTGCAGCTCTCCACCCCTTGACAATCTTACAGGGGTGAGAGAAAACATTTTTTAACACCTTG 141
Qy 25 LeuLeuTyrProValSerAspSer----- 32
Db 142 TTAGTCTACAATGCCTCAGACAGAGTTTCCGTAGATCCTGCAAAAAGTAATTCGGCAGGCT 201
Qy 33 ---SerGlnTyrProThrIleValSerThrPheGluGlnGlyLeuLysArgPheSerGlu 51
Db 202 CTCTCCAGAGTGTGGTACTACTATTCCTTTTCAGGGCGTCTCAGAAAAAGAAAT 261
Qy 52 AlaValProTrpValalaGlyGlnValLysAlaGluGlyIleSerGluGlyAsnThrGly 71
Db 262 -----GGAGATCTTGAAGTGGAGTGCACAGGGGAG-----GCT 294
Qy 72 ThrSerPheIleValProPheGluAspValProArgValValValLysAspLeuArgAsp 91
Db 295 GCTCTGTGTGGAAAGCCATGGCTGACACTGACCTCTCAGTCTTAGGAGATTTG----- 348
Qy 92 AspProSerAlaProThrIleGluGlyMetArgLysAlaGlyTyrProMetAlaMetPhe 111
Db 349 GATGACTACAGTCCCTTCACTTGAGCACTA-----CTTTT 384
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Qy 152 ValAsnGlyGlnHisGlyValaMetAspMetValGlyGlnAspAlaValIleArgLeuLeu 171
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Qy 172 SerLysAlaCysArg-----AsnAspProPheThrGluGluMet 185
Db 532 CGAGAGATGGCAAGGGAGAGATTAAAGCCTCTCGAGCCAATATGGAAGAGAGAAATTG 591
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Qy 206 ProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThr 225
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Qy 226 ProValSerAlaSerTrpAlaPheThrPheSerProLysAlaMetSerGluLeuLys 245
Db 697 -----TCTGAGACAATA 708
Qy 246 AspAlaAlaThrLysThrIleu-----AspAlaSerThrLysPheValSerThrAspAla 264
Db 709 AATTGTATCAAAACAATGCTTAGGGAAGAAAGAAATTTTGCTCTCGCTGAGGTT 768
Qy 265 LeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySer 284
Db 769 GTATCTGCATTTGGCTGG-----ATAGCAAGCAAGGGCTCTTCAAAATTCACATAGT 322
Qy 285 AlaProThrGluPheCysArgAlaValaAspAlaAArgProAlaMetGlyValSerAsnAsn 304
Db 823 GAGAAATGTGAAGCTTATTTTTCATATGGACATGAGAAAATTTATTAAT----- 870
Qy 305 TyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGluIle----- 322
Db 871 ---CCACCACCTTTCGAAGGGA-----TACTACGGTAATTTTGTGGTACCCTATGTGCA 921
Qy 323 -----AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAsp 339
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QY 396 LysProGluThrValArgArgProIlePheGluProValGluSerLeuMet---TyrPhe 414
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Job time : 173 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2334	100.0	1356	16	US-10-614-954-5	Sequence 5, Appli
3	1860.5	79.7	1403	13	US-10-074-279-1	Sequence 1, Appli
4	1860.5	79.7	1403	16	US-10-614-954-1	Sequence 1, Appli
5	1860.5	79.7	12949	13	US-10-074-279-11	Sequence 11, Appl
6	1860.5	79.7	12949	16	US-10-614-954-11	Sequence 11, Appl
7	1860.5	79.7	13737	13	US-10-074-279-10	Sequence 10, Appl
8	1860.5	79.7	13737	16	US-10-614-954-10	Sequence 10, Appl
9	962.5	41.2	1425	13	US-10-074-279-7	Sequence 7, Appli
10	962.5	41.2	1425	16	US-10-614-954-7	Sequence 7, Appli
11	445.5	19.1	695	18	US-10-653-047-4594	Sequence 4594, Ap
12	191	8.2	2235	18	US-10-425-115-160676	Sequence 160676,
13	187.5	8.0	1341	17	US-10-437-963-75946	Sequence 75946, A
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18	170.5	7.3	1587	13	US-10-078-929-63	Sequence 63, Appl
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21	165	7.1	1721	17	US-10-437-963-44166	Sequence 44166, A
22	161	6.9	1556	13	US-10-078-929-59	Sequence 59, Appl
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26	157.5	6.7	1296	17	US-10-437-963-62509	Sequence 62509, A
27	157.5	6.7	3424	16	US-10-424-599-118915	Sequence 118915,
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38	143	6.1	1428	9	US-09-938-842A-1390	Sequence 1390, Ap
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41	142.5	6.1	1765	16	US-10-424-599-134525	Sequence 134525,
42	142	6.1	1347	9	US-09-866-570A-55	Sequence 55, Appl
43	142	6.1	1347	9	US-09-866-570A-55	Sequence 55, Appl
44	142	6.1	1347	15	US-10-166-984-55	Sequence 55, Appl
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ALIGNMENTS

RESULT 1  
US-10-074-279-5  
; Sequence 5, Application US/10074279  
; Publication NO. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencecellat  
; CURRENT APPLICATION NUMBER: US/10/074,279  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/538,414  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5

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; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

Alignment Scores:
Pred. No.: 1.14e-267 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

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QY 201 AsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGly 220
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RESULT 2

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; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-614-954-5
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Alignment Scores:
Pred. No.: 1.14e-267 Length: 1356
Score: 2334.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
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DB 1 ATGGCTTTCAAGATACAGTCGACACCCCTCGGCCAGCTACCAAGCCCTCTTTTCGATCTAC 60
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 QY 281 IleAspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGly 300  
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RESULT 3  
 US-10-074-279-1  
 ; Sequence 1, Application US/10074279  
 ; Publication No. US20020162136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hohn, T.  
 ; APPLICANT: Salmeron, J.  
 ; APPLICANT: Peters, C.  
 ; APPLICANT: Kendra, D.  
 ; APPLICANT: Reinders, J.  
 ; APPLICANT: Kuznia, R.  
 ; APPLICANT: Dill-Mackey, R.  
 ; TITLE OF INVENTION: Transgenic Plant and Methods  
 ; FILE REFERENCE: sequencelist  
 ; CURRENT APPLICATION NUMBER: US/10/074,279  
 ; CURRENT FILING DATE: 2002-02-12  
 ; PRIOR APPLICATION NUMBER: US/09/538,414  
 ; PRIOR FILING DATE: 2000-03-29  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1403  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium sporotrichioides  
 US-10-074-279-1

Alignment Scores:  
 Pred. No.: 3,46e-211 Length: 1403  
 Score: 1860.50 Matches: 349  
 Percent Similarity: 88.67% Conservative: 50  
 Best Local Similarity: 77.56% Mismatches: 50  
 Query Match: 79.71% Indels: 1  
 DB: 13 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-1 (1-1403)

QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21  
 DB 37 TCTTTTGAATAGAGTCGACATCATCGGCGCAGCAACCGCTCTTCTTCAATCTACAC 96  
 QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41  
 DB 97 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCACC 156  
 QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61  
 DB 157 CTTGAGAGGCGCTAAAGCGCTCTCTCAACCTTCCATGCGTGGCGCGGCGGCAAG 216  
 QY 62 AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81  
 DB 217 ACCGAGGATCAGCGAAGAAACACAGGAACCTTCCAGATCAITCCATATGAGGAGACA 276  
 QY 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101  
 DB 277 CCCCCTGTGTGTGAAGACCTCCGTCGATGATTCCTCAGCGCCACGATCGAGGGGTG 336  
 QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121

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Db 337 AGAAGGCGGGTTTCCCTTAGAGATGTTTTCAGAGAACGTCGTCGCGAGGAAGACA 396
Qy 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 397 TTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAAGCCTGTGTGCTATTGCGAGCTC 456
Qy 142 AsnPhelIleLysGlyGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 457 AACTTCATTAAAGGCGGAGCTCATCTTCACGTCACGGACCAACATGGTGCTATGGACATG 516
Qy 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
Db 517 ACAGGACAGATCAATATTATCTCTCTCCAAAGCGTGGCCGCAACGAATCATTCACC 576
Qy 182 GluGluGluMetThrAlaMetAsnLeuLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 577 GAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCTCTCTCTTGAAGAAC 636
Qy 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAAGTTGGTCTCTGAGCTAGACACCAACAGATCGCCAAACCTCGCGCTGCT---GGCGAC 693
Qy 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 694 GCTCCACCGCGACCGGCCAAGGCAAGCTGGCGCTCTTTTCAATTCATCTCCCAAGGCGCTC 753
Qy 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 754 TCGGAGCTGAAGACCGCAGCCCAAGACTCTTGACGCGTCGTCGAAGTTGTGTCAACT 813
Qy 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTAAGTCTCGCAAGATTG 873
Qy 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 874 GATGCTTCCACACACTACTGAATTTCTCGCGCTGTGCGACATGCGGGGCCCAATGGCGTA 933
Qy 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAAGCACATACCCAGGCTCTTCAAAACATGACCTACATGACTCGACCTCGGCCGAA 993
Qy 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCAACGAACCACTTGGCGCAACAGCATCAGCGCTGCGCTCGGAACCTCAACAGTGAT 1053
Qy 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1054 CGTTTCGCGACAGCAACAGCTTTGGCGACGCTACATGCTATGCTGCGCTGCAAGATCG 1113
Qy 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCTGACCCCGATGGAAATCCGTCAAGCAGCATGATGCTGAGTTCTCTGGGCC 1173
Qy 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGTTCGGATGCTGGGAGTATGACTTTGGGTTTGGAGTGGTAAAGCCTGAGAGTGTGAGA 1233
Qy 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTTGAACCTTTTGAGAGTTTGATGCTTTATGTCCTTGAAGAGCCCTGATGGG 1293
Qy 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1294 GAGTTTACCGCGTCCATTTCTCTGAGGGATGAGGATATGAGAGACTAAAGCGGATGAG 1353
Qy 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGGACAAAGTACGCAAGTATATTGGG 1383
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RESULT 4

US-10-614-954-1

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; Sequence 1, Application US/10614954
; Publication No. US20040034884A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/614,954
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
; US-10-614-954-1
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## Alignment Scores:

Pred. No.:	3,46e-211	Length:	1403
Score:	1860.50	Matches:	349
Percent Similarity:	88.67%	Conservative:	50
Best Local Similarity:	77.56%	Mismatches:	50
Query Match:	79.71%	Indels:	1
DB:	16	Gaps:	1

US-10-614-954-6 (1-451) x US-10-614-954-1 (1-1403)

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Qy 2 AlaPheLysIleGleLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 37 TCTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCCTCTCTTTCAATCTACACC 96
Qy 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 97 CAGATCAGTCTCGTTTACCCCTCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 156
Qy 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys 61
Db 157 CTTGAGGAGGCGCTAAACCGCTCTCTCAACCTTCCCATGGGTGCGGGCCAGGTCAAG 216
Qy 62 AlaGluGlyIleSerGluLysAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 217 ACCGAGGCGCATCAGCGAAGAAACACAGAACTTCCAAGATCATTCATATGAGGAGACA 276
Qy 82 ProArgValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 277 CCCCGTCTTGTGTGAAGACCTCGGTGATGATCTCTCAGCGCCCAACGATCGAGGGGTG 336
Qy 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleAlaProArgLysThr 121
Db 337 AGAAGGCGGGTTTCCCTTAGAGATGTTTTCGAGAGACGTCGTCGCTCCGAGGAGACA 396
Qy 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 397 TTAGCTATCGGACCTGGCAATGGCCCAACGACGAGCCTGTGTGCTATTGCTATGAGCTC 456
Qy 142 AsnPhelIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 457 AACTTCATTAAAGGCGGAGCTCATCTTCACGTCACGGACCAACATGGTGCTATGGACATG 516
Qy 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
Db 517 ACAGGACAGATGCAATATTATCTCTCTCTCAAGCGGTGCGCAACGAATCATTCACC 576
Qy 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 577 GAGGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCTCTCTCTCTTGAAGAAC 636
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QY 202 TyrThrIleGlyProGluValAspHisGlnIleValIysAlaAspValAlaGlyGlyAsp 221
Db 637 TACAAGTTGGTCTCGCTAGCTAGACCAACAGATCCCAAACTCGGCTGCT--GGCGAC 693
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProIysAlaMet 241
Db 694 GCTCCACCGCAGCGGCAAGCAAGCTGGCGCTCTTTTTCATCTACCTCCCAAGGCCCTC 753
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 754 TCGAGCTGAAAGCGCAGCACCAGAGACTCTTGACCGCTGCTCCAAAGTTTGTCTCACT 813
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 814 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 873
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 874 GATGCTTCCACACCTACTGAATTTCTCCGCGCTGTGCACATGCGGGGCCCAATGGGCGTA 933
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 934 TCAAGACATACCCAGCGCTTCTTCAAACATGACCTACCATGACCTGACCGCTCGCGCAA 993
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 994 ATCGCAACGAACCACTTGGCGCAACAGCATCAGCGCTCGGCTCGGAACCTCAACAGTGAT 1053
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1054 CGTTTCGCGCAGAGAAACACAAGCTTTGGCGACGTACATGATGCGCTCGCTGCAAGTCG 1113
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTrpAla 381
Db 1114 AGCGTCTCCCTGACCGCGGATGGATCCGTCAAGCAGCATCATGCTGAGTTCTGGGCC 1173
QY 382 LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1174 AAGTGGGATGCTGGGAGTATGACTTTGGTGGTAAAGCTGAGAGTGTGAGA 1233
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1234 AGACCTCGCTTTGAACCTTTGAGAGTTTGTATGTACTTTATGCCCCAAGAAGCCTGATGG 1293
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1294 GAGTTTACGGCGTCCATTTCTTGAGGGATGAGGATATGAGAGACTTAAGCGCGATGAG 1353
QY 442 GluTrpThrLysTyrAlaGlnTyrValGly 451
Db 1354 GAGTGGCAAAAGTACGCAAGTATATTGGG 1383
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## RESULT 5

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US-10-074-279-11
; Sequence 11, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/539,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Alignment Scores:
Pred. No.: 1,03e-209 Length: 12949
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservative: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 13 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-11 (1-12949)

QY 2 AlapheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 11282 TCYTTTGCATAGAGCTCGACATCATCGGCAGCAACCGCTCTTCTTCAATCTACACC 11341
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 11342 CAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCACCATCGTCAGCACC 11401
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProTrpValAlaGlyGlnValLys 61
Db 11402 CTTGAGGAAGGCCATAAAGCGCTCTCTCAAACTTCCCATGGTCCGCGGCCAGGTCAAG 11461
QY 62 AlaGluGlyLysSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal 81
Db 11462 ACCGAGGATCATGCGAAGAAACACAGGAACCTTCAAGATCAITCCATATGAGGAGACA 11521
QY 82 ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet 101
Db 11522 CCCCCTGTTGTTGGTGAAGACCTCCGCTGATGATTCCTCAGCGCAACGATCGAGGGTTG 11581
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 11582 AGAAAGCGGGTTTCCCTTAGAGATGTTTTCAGCAGAACCTCGCTCGCGAGGAAGACA 11641
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 11642 TTAGCTATCGACCTGGCAATGCCCCACGACCCGAGGCTGTGTGCTATTCGAGCTC 11701
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 11702 AACTTCATTAAGGCGGAGCTCATTCCTCAGCGTCAACGGCAACATGGTGTATGGACATG 11761
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr 181
Db 11762 ACAGCAAGATGCAATTATTCTCTTCTCAAGGCGTCCGCAACGAATCATTCACC 11821
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 11822 GAGGAGGAATCTCGGCCATGAACTCGATCGCAAGACGGTAGTCCCTCTCCTTGAANAAC 11881
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 11882 TACAAAGTTGGTCTCTGAGCTAGACCAACCATCGATCGCCAAACCTCGCCCTGCT--GGCGAC 11938
QY 222 AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet 241
Db 11939 GCTCCACCCGACCGCAAGCAAGCTGGCGCTCTTTTTCATTCATCCCAAGGCCCTC 11998
QY 242 SerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 11999 TCGAGCTGAAAGCGCAGCACCAGAGACTCTTGACGCGTCTGCGCAAGTTTGTCAACT 12058
QY 262 AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle 281
Db 12059 GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 12118
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
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QY 382 LysValGlyLeuThrPaspTyrPaspPheGlyLeuGlyLeuGlyProGluThrValArg 401
Db 12419 AAGTGGGATGCTGGGAGTATGACTTTGGGTTGGAGCTGGTAAGCCTGAGAGTGTGAGA 12478
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 12479 AGACTCGCTTGAACCTTTGAGAGTTGATGATCTTTATGCCCAAGAGCCTGATGGG 12538
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 12539 GAGTTTACGGCGTCCATTCTCTGAGGATGAGGATATGAGAGACTAAGGCGGATGAG 12598
QY 442 GluThrThrLysTyrAlaGlnTyrValGly 451
Db 12599 GAGTGACAAAGTACGCAAAAGTATATTGGG 12628

RESULT 7
US-10-074-279-10
; Sequence 10, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-10-074-279-10

Alignment Scores:
Pred. No.: 1,13e-209 Length: 13737
Score: 1860.50 Matches: 349
Percent Similarity: 88.67% Conservatives: 50
Best Local Similarity: 77.56% Mismatches: 50
Query Match: 79.71% Indels: 1
DB: 13 Gaps: 1

US-10-614-954-6 (1-451) x US-10-074-279-10 (1-13737)
QY 2 AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr 21
Db 51 TCTTTTGACATAGAGCTCGACATCATCGCCAGCAACCGCTCTTCTTTCAATCTACACC 110
QY 22 GlnIleSerLeuLeuTyrProValSerAspSerSerGlnTyrProThrIleValSerThr 41
Db 111 CAGATCAGTCTCGTTTACCCCGCTCTGATCCCTCCAGTATCCCAACCATCGTCAGCACC 170
QY 42 PheGluGlnGlyLeuLysArgPheSerGluAlaValProIleValAlaGlyGlnValLys 61
Db 171 CTTGAGGAAGGCTTAAAGCCCTCTCTCAAACTCCCATGGTCCGCGCCAGGTCAG 230
QY 62 AlaGluGlyIleSerGluGlyAserThrGlyThrSerPheIleValProPheGluAspVal 81
Db 231 ACCGAGGGCATCAGCGCAAGAAACACAGGAACCTTCCAAGATCATTCCATATGAGGAGACA 290
QY 82 ProArgValValValLysAspLeuArgAspProSerAlaProThrIleGluGlyMet 101
Db 1368 GAGTGACAAAGTACGCAAAAGTATATTGGG 1399
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Db 291 CCCGCTCTTGGTGAAGACCTCCGCTGATGATTCCTCAGCGCCAAAGCATCGAGGGGTG 350
QY 102 ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr 121
Db 351 AGAAAGCGGGTTTCCCTTTAGAGATGTTTTCAGGAGAACTGCTGCTCCGAGGAAAGACA 410
QY 122 LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu 141
Db 411 TTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAACTGTGTGTTATTTCGAGCTC 470
QY 142 AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet 161
Db 471 AACTTCATTAAAGGCGGACTCATTTCTACCGTCAACGGACACATCGTGTGATGGACATG 530
QY 162 ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPropheThr 181
Db 531 ACAGGACAAGATGCAATTATTCTCTCTCCAGGCGTCCGCAACGAATCATTTCCACC 590
QY 182 GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn 201
Db 591 GAGGAGGAAATCTCGGCCCATGAACCTCGATCGCAAGACGGTAGTCCCTCTCTTTGAAAC 650
QY 202 TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp 221
Db 651 TACAAGTTGGTCTGTGAGTAGACACACAGATCGCCAAACCTCGCGCTGCT---GGCGAC 707
QY 222 AlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLysAlaMet 241
Db 708 GCTCCACCCGACCGGCCCAAGCAAGCTGGCGGTTCTTTTTCATTCTACTCCCAAGGCCCTC 767
QY 242 SerGluLeuLysAspAlaIleThrLysThrLeuAspAlaSerThrLysPheValSerThr 261
Db 768 TCGGAGCTGAAAGACGACGACCAAGACTCTTGACGCGTCTGTCGAAGTTTGTGTCAACT 827
QY 262 AspAspAlaLeuSerAlaPheIleTyrLysSerAlaSerArgValArgLeuGluArgIle 281
Db 828 GATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGCTAGCTCTCGCAAGATTG 887
QY 282 AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal 301
Db 888 GATGCTTCCACACCTACTGAAATTTTCGCGCGCTGTGACATGCGGGGCCCAATGGGCGTA 947
QY 302 SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu 321
Db 948 TCAAGCACATACCCAGGCTTCTTCAAAACATGACCTACCATGACCTCGACCGCTCGCGAA 1007
QY 322 IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla 341
Db 1008 ATCCCAACGAACCACTTGGCGCAACAGCATCACGCTCGCTCGGAACTCAACAGTGAT 1067
QY 342 SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer 361
Db 1068 CGTTTGGCGAGACGAACACAAAGCTTTGGCGCGTACATGATGCTGCTGCTGACAAAGTCG 1127
QY 362 AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyrAla 381
Db 1128 AGCGTCTCTCGCCCGCATGCGATCGTCAAGCAGCATCATGCTGAGTTCCTCGGGCC 1187
QY 382 LysValGlyLeuTyrAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg 401
Db 1188 AAGGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAGCTGAGAGTGTGAGA 1247
QY 402 ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly 421
Db 1248 AGACCTCGCTTTGAACCTTTTGGAGTGTGATGATCTTTATGCCCCAAGAGCCTGATGG 1307
QY 422 GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys 441
Db 1308 GAGTTTACGGCGTCCATTCTCTGAGGGATGAGGATATGAGAGACTAAGGCGGATGAG 1367
QY 442 GluThrThrLysTyrAlaGlnTyrValGly 451
Db 1368 GAGTGACAAAGTACGCAAAAGTATATTGGG 1399
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## RESULT 8

US-10-614-954-10  
; Sequence 10, Application US/10614954  
; Publication No. US20040034864A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/614,954  
; CURRENT FILING DATE: 2003-07-07  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 13737  
; TYPE: DNA  
; ORGANISM: Plasmid  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
US-10-614-954-10

Alignment Scores:  
Pred. No.: 1,13e-209 Length: 13737  
Score: 1860.50 Matches: 349  
Percent Similarity: 88.67% Conservative: 50  
Best Local Similarity: 77.56% Mismatches: 50  
Query Match: 79.71% Indels: 1  
DB: 16 Gaps: 1

US-10-614-954-6 (1-451) x US-10-614-954-10 (1-13737)

QY	2	AlaPheLysIleGlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThr	21
DB	51	TCCTTTGACATAGATCGACATCATCGGCAGCAACCGCCTCTCTTCAATCTACACC	110
QY	22	GlnIleSerLeuLeuTyrProValSerAspSerGlnTyrProThrIleValSerThr	41
DB	111	CAGATCAGTCTGTTTACCCCGTCTCTGATCCCTCCAGCATCCACCATCGTCAGCACC	170
QY	42	PheGlnGlnGlyLeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLys	61
DB	171	CTTGAGGAAGGCTAAAGCGCTCTCTCAACCTTCCCATGGTGGTCCGGCGCCAGGTCAAG	230
QY	62	AlaGluGlyIleSerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspVal	81
DB	231	ACGAGGGCATCAGCGAAGAAACAAGAACTTCCCAAGATCATTCATATAGGAGACA	290
QY	82	ProArgValValValLysAspLeuArgAspAspProSerAlaProThrIleGluGlyMet	101
DB	291	CCCCGTCTGTGTGAAGACCTCGTGATGATTCCTCAGCGCAACGATCGAGGGGTG	350
QY	102	ArgLysAlaGlyTyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThr	121
DB	351	AGAAAGCGGGTTCCTCCCTTAGAGATGTTTACGAGAACGTCGTCGTCGAGGAAGACA	410
QY	122	LeuProIleGlyProGlyThrGlyProAspAspProLysProValIleLeuLeuGlnLeu	141
DB	411	TTAGCTATCGGACCTGGCAATGCCCAACGACCGGAGCGCTGTGTGTATTCGAGCTC	470
QY	142	AsnPheIleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMet	161
DB	471	AACTTCATTAAAGGCGGACATCTCTCACCCTCAACGGACACATCGTGTATGGACATG	530
QY	162	ValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThr	181

DB	531	ACAGGACAAGATGCAATTATTTCCTCTCTCCAGGCGTGGCGCAACGAATCATTCACC	590
QY	182	GluGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsn	201
DB	591	GAGGAGAAATCTGGCCATGAACCTCGATCGCAAGCGGTAGTCTCTCTTTGAAAAC	650
QY	202	TyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGlyGlyAsp	221
DB	651	TACAAAGTTGGTCTCGAGCTAGACCAACAGATCGCCAAACCTCGCGCTGTCT---GGCGAC	707
QY	222	AlaValLeuThrProValSerAlaSerTrpAlaPhePheThrPheSerProLysAlaMet	241
DB	708	GCTCCACCGCGCACCGCCCAAGCAGCTGGGGTCTTTTTCATTCATCCCAAGGCGCTC	767
QY	242	SerGluLeuLysAspAlaIleThrLysThrLeuAspAlaSerThrLysPheValSerThr	261
DB	768	TCGAGCTGAAGACCGCACCAAGACTCTTGCGCGTGTGCGCGTGTGCTCAAGTTTGTCACT	827
QY	262	AspAspAlaLeuSerAlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIle	281
DB	828	GATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGCTCGCAAGATTG	887
QY	282	AspGlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMetGlyVal	301
DB	888	GATGCTTCCACACCTACTGAATCTGCGCGCTGTGACATCGCGGGGCCCAATGGCGTA	947
QY	302	SerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIleGlyGlu	321
DB	948	TCAGCACATACCCAGGCGCTTCTTCAAAACATGACCTACATGATCGACCTCGCGCGAA	1007
QY	322	IleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAla	341
DB	1008	ATCGCAACGAACCACTTGGCGCAACAGCATCACGCTCGGCTCGGAATCAACAGTGAT	1067
QY	342	SerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsnProAspLysSer	361
DB	1068	CGTTTCGCGCAGACGAACACAGCTTTGGCGAGCTACATGATCGCTGCGCTGACAAAGTCG	1127
QY	362	AsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerSerTyrAla	381
DB	1128	ACGCTCTCCCTGACCGCGCATCGAATCCGTCAAGCAGCATCATGCTGAGTTCCTGGGCC	1187
QY	382	LysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrValArg	401
DB	1188	AAGTGGGATGCTGGGAGTATGACCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1247
QY	402	ArgProIlePheGluProValGluSerLeuMetTyrPheMetProLysLysProAspGly	421
DB	1248	AGACCTCGCTTTGAACCTTTTGAAGATTTGATGTATCTTTATGCCCAAGAGCCTGATGG	1307
QY	422	GluPheCysAlaAlaLeuSerLeuArgAspGluAspMetAspArgLeuLysAlaAspLys	441
DB	1308	GAGTTTACGGCTTCATTTCTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG	1367
QY	442	GluTyrThrLysTyrAlaGlnTyrValGly	451
DB	1368	GAGTGACAAAGTACGCAAGTATATTGGG	1397

## RESULT 9

US-10-074-279-7  
; Sequence 7, Application US/10074279  
; Publication No. US20020162136A1  
; GENERAL INFORMATION:  
; APPLICANT: Hohn, T.  
; APPLICANT: Salmeron, J.  
; APPLICANT: Peters, C.  
; APPLICANT: Kendra, D.  
; APPLICANT: Reinders, J.  
; APPLICANT: Kuznia, R.  
; APPLICANT: Dill-Mackey, R.  
; TITLE OF INVENTION: Transgenic Plant and Methods  
; FILE REFERENCE: sequencelist  
; CURRENT APPLICATION NUMBER: US/10/074,279

; CURRENT FILING DATE: 2002-02-12  
 ; PRIOR APPLICATION NUMBER: US/09/538,414  
 ; PRIOR FILING DATE: 2000-03-29  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1425  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces cerevisiae  
 US-10-074-279-7

Alignment Scores:  
 Pred. No.: 4,26e-104 Length: 1425  
 Score: 962.50 Matches: 202  
 Percent Similarity: 62.86% Conservative: 84  
 Best Local Similarity: 44.40% Mismatches: 158  
 Query Match: 41.24% Indels: 11  
 DB: 13 Gaps: 8

US-10-614-954-6 (1-451) x US-10-074-279-7 (1-1425)

Qy	6	GlnLeuAspThrLeuGlyGlnLeuProGlyLeuLeuSerIleTyrThrGlnIleSerLeu	25
Db	64	CACTTGGATATTTGGGACACACCTTCGCTATACAACTATACACTCAATATGCTCT	123
Qy	26	LeuTyrProValSerAspSerGlnTyrProThrIleValSerThrPheGluGlnGly	45
Db	124	ATCTACCGTGATACAGATCCTTCTGCTCATGACCATATCGTAATACCTTAACAAGAGA	183
Qy	46	LeuLysArgPheSerGluAlaValProTyrValAlaGlyGlnValLysAlaGluGlyIle	65
Db	184	CTTGAACAACTTGGCTAAAAAATTTCCAGTGGCTAGCAGGAAATGTCTAAATGAAGTGTCT	243
Qy	66	SerGluGlyAsnThrGlyThrSerPheIleValProPheGluAspValProArgValVal	85
Db	244	GACGAAGTTAACACTGGTACCTACGAATGTCCGCTAGACAAATTTCCA---CTTATC	300
Qy	86	ValLysAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAlaGly	105
Db	301	GTCCAAAGATCTTCGAGAAGATCTGTCTGCCCAACAATGGATTCGCTTGAAGAAAGCTGAC	360
Qy	106	TyrProMetAlaMetPheAspGluAsnIleIleAlaProArgLysThrLeu---Profile	124
Db	361	TTTCTCTATCTACATGTTAGACGAAAGACATTTTGGCGCTTGACACTATCAATCCACCT	420
Qy	125	GlyProGlyThrGly---ProAspAspProLysProValIleLeuLeuGlnLeuAsnPhe	143
Db	421	GGAAACACTATAGTATGGCGCGCAAGATGGCGCTGTATTTGGCAGTTCAAGCAAACTTT	480
Qy	144	IleLysGlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGly	163
Db	481	ATCTCCGGCGGCTCGCTTAACTATTGTTCGGCGACCAATATATTGATATACACAGA	540
Qy	164	GlnAspAlaValIleArgLeuSerLysAlaCysArgAsnAspProPheThrGluGlu	183
Db	541	CAGAAAGTATCATCAACTTGCTCAATAAATCTTGCACCAAAAACCTTTCTCTGATGAA	600
Qy	184	GluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeuGluAsnTyrThr	203
Db	601	GAACCTGCTCAATTGGAATATAGATAAAGCAAACTTATTCCTTTGTTGATGAA---ACT	657
Qy	204	IleGlyProValLeuAsp-----HisGlnIleValLysAla-----AspValAlaGly	219
Db	658	TGGGAACCCGACACACCGCTAGTTTCATGAATAGTGGAAACCTCTAGAAATACAGTGA	717
Qy	220	GlyAspAlaValLeuThrProValSer---AlaSerTrpAlaPhePheThrPheSerPro	238
Db	718	GAGGAAAAGGAACAGCTTGTCTTCGAACTCTACTTGGGCTTATGTTGAATTTCTGCT	777
Qy	239	LysAlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPhe	258
Db	778	ATCTCATTTGCAATCTGAGGATTTTGGCAATGACAGACATGTACTTCTGGCACAATAATTT	837

[illegible]

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Db      231  GGCTCGAAGACTGTCACCAATTTCCCTGGGTAGCAGCCAGATAGTCAGTGAAGGC 230
QY      65  ILeSerGluGlyAenThrGlyThrSerPheileValProPheGluAspValProArgVal 84
Db      291  AGCAGCCACAAATCCTGGCACAATTCATGATCAAGAGCACTGGGGAAGACTCCACCACTG 350
QY      85  valVallyAspLeuArgAspProSerAlaProThrIleGluGlyMetArgLysAla 104
Db      351  GTTGTGAAGACTTCCGTATGATCCGACGTTCCGACCATGAGCATTTGAGACGCGCC 410
QY      105  GlyTyPProMetAlaMetPheAspGluAsnIleAlaProArgLysThrLeuProIle 124
Db      411  GACTTTCCCTTTCGGATGTAGACGAGAACATCTCTCGAAGAACCTTGCCA--- 467
QY      125  GlyProGlyThrGlyProAspPro-----LysProValIleLeuLeuGlnLeuAsn 142
Db      468  -----AGCCCTGAGGAAGATATTATCTACCGCGCTTCTTGTGCCAGGCTAAT 515
QY      143  PheIleIysGlyLeuLeuLeuThrValAsnGlyGlnHisGlyAlaMetAspMetVal 162
Db      516  TWTATTACGGCGGCTGGTCTCACTCTTTGTGGCCATCATAGCACAAATGGACATGACT 575
QY      163  GlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGlu 192
Db      576  GGTGANGGACAGGTATCCACCTTCTCTGAGGAGCATGTCGTGGGATACATATACAAGA 635
QY      183  GluGluMetThrAlaMetAsnLeuAspArgLysThrIleValPro 197
Db      636  TTGGAGCTAGAGTCAGGAGACTTAATGAAGGTCACTCGTTGCC 680

RESULT 12
US-10-425-115-160676
; Sequence 160676, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160676
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78117C.1
US-10-425-115-160676

Alignment Scores:
Pred. No.:      8,4e-12      Length:      2235
Score:          191.00      Matches:     110
Percent Similarity: 38.29%      Conservative: 60
Best Local Similarity: 24.77%      Mismatches: 219
Query Match:      8.18%      Indels:      55
DB:              18          Gaps:         16

US-10-614-954-6 (1-451) x US-10-425-115-160676 (1-2235)

QY      13  LeuProGlyLeuLeuSerIleTyThrGlnIleSerLeuLeuTyProValSerAspSer 32
Db      463  CTCCCTACATACCTTCTACTACACCAAGAGCTCTCTGTACCGGCC-----GCC 516
QY      33  SerGlnTyProThrIleValSerThrPheGluGlnGlyLeuLysArgPheSerGluAla 52
Db      517  CCCGACTTCCCGGACCGCTGGGGCCATGACGGCCGCGCTGCCACCGGCTCCGCGTC 576
QY      53  ValProTrpValAlaGlyGlnValLysAlaGluGlyIleSerGluGlyAsnThrGlyThr 72
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Db      577  TTCTACCCGCTGCTCCGCGCATTCGCCAGGAC-----GACGGCGGC 618
QY      73  SerPheIleValProPheGluAsp-ValProArgValValValLysAspLeuArgAspAs 92
Db      619  GCCTCGCGCTTGAGGCGGACGAGGCGCGCGAGGTCTTCGAGCGCGGCGGCCGCGTC 678
QY      92  pProSerAla-ProThrIleGluGlyMetArgLysAlaGlyTyProMetAlaMetPheA 112
Db      679  GCCTCGAGCAGACTCCGCGGAGGGGACTCGCAGCAGGAGC-----G 720
QY      112  spGluAsnIleIleAlaPro-----ArgLysThrLeuProIleGlyProGlyT 128
Db      721  GAGAAGGTCTTGAGCAGACCTCGTGCCTACCGCGGTCTATGAACCTTCGAGGGCCT--- 776
QY      128  hrGlyProAspAspPro-LysProValIleLeuLeuGlnLeuAsnPheIleLysGlyGly 147
Db      777  -----CCGCGCGCGCTTCTCGCGTCCATTTACAAAGCTCAAGGAGCGT 822
QY      148  LeuIleLeuThrValAsnGlyGlnHisGlyAlaMetAspMetValGlyGlnAspAlaVal 167
Db      823  CTGGCGGTGGGTGGCGCTTCAACACACGCGGTCTGCACGCGCACCTCCACGTGCACATC 882
QY      168  IleArgLeuLeuSerLysAlaCysArgAsnAspProPheThrGluGluMetThrAla 187
Db      883  ATGTCTCATGGCGGAGCTCTGCCGCGGTACCCCTGTCTGCTGCAGCCCATCCACGAC 942
QY      188  MetAsnLeuAspArgLysThrIleValProTyLeuGluAsnTyThrIleGlyProGlu 207
Db      943  CGGTCTCTGTCGCTCCGTCGCGGTG---CGCTGAGCTG-----CCGGCG 987
QY      208  ValAspHisGlnIleValLysAlaAspValAlaGlyGlyAspAlaValLeuThrProVal 227
Db      988  TCCGCGGAGGCCACGAGAAGACGAGCCGACGCGCGGCGGCGGCTGGTGCGC--- 1044
QY      228  SerAlaSerTrpAlaPhePheThrPheSerProLysAlaMetSerGluLeuLysAspAla 247
Db      1045  -----CGCGTCTTCTGTTCCCGAGCCACCGCTGGCGCGCATCAAGCGCGCG 1092
QY      248  AlaThrLysThrLeuAspAlaSerThrLysPheValSerThrAspAspAlaLeuSerAla 267
Db      1093  GCCAACGCGCGCTGCGCGCGCGCGGCGGCAAGCCCTTCTCAGTTCAGTCCCTCGGGGCG 1152
QY      268  PheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaPro--- 286
Db      1153  CATCTCTGGCGCGCTCTCCGCGCGCGG-----GGCTCGCGCCCGCC 1197
QY      287  -----ThrGluPheCysArgAlaValAspAlaArgProAlaMetGly-----ValSer 302
Db      1198  GACATCACCGCTTTCGCGCTTTCGCGGACTGCGCGCGCGCTCGACCGCCCTCCCG 1257
QY      303  AsnAsnTyProGlyLeuLeuGlnAsnMetThrTyHisAsnSerThrIleGlyGluIle 322
Db      1258  CCGGCTACTTCGGCAACCTCATCGAGCGGTGTTCACGGCGGTGTCGCGGGGATGCTC 1317
QY      323  AlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSer 342
Db      1318  CTGGGCGGCGCCCGAGCTGCGCGCGGCTCTGCTGAGAGGCCATCGACGAGCAGCAG 1377
QY      343  MetArgGlnArgThrArgGlyLeuAlaThrTyLeuHisAsnAsnProAspLysSerAsn 362
Db      1378  GCCGCGCGCTCACGAGGAGGTGGAGGAGTAC---GAGCGCGCGCGCCCAAGCTGTTCAC 1434
QY      363  ValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeuSerTrpAlaLys 382
Db      1435  TACAGC-----GACCGCGCGCCCAAC---TGGCTGCGCTCGGAGCTCGCGCGCG 1482
QY      383  ValGlyLeuTrpAspTyAspPheGlyLeuGlyLeuGlyProGluThrValArgArg 402
Db      1483  TTCAGGCTTACAGCTCGACTTC-----GGCTCGGAGCGCGCGCGCTCCGCGAGC 1536
QY      403  ProIlePheGluProValGluSerLeuMetTyPheMetPro---LysLysProAspGly 421
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Qy 207 GluValAspHisGlnIleValVallysAlaAaspValalaGlyGlyAspAlaValLeuThrPro 226  
Db 713 ATTTTGGATCACATTTGAATAACAAGCCCAACAGCATGAAGACTAACAGCTACTAAAT 772  
Qy 227 ValSerAlaSerTrpAlaPhePheThrPheserProlysAlaMetSerGluLeuLysAsp 246  
Db 773 GCATCAGCAGCTGTCTATTTCAGACTCAGCGGTACCAGCTCAACACACACTGAAA--- 829  
Qy 247 AlaAlaThrLysThrLeuAlaSerThrLysPheValSerThrAspAlaLeuSer 266  
Db 830 ---GCCAAATCCAAGAAGATGCCAACACAACTAGCTATAGTCTTATGAGATGTGGCG 886  
Qy 267 AlaPheIleTrpLysSerAlaSerArgValArgLeuGluArgIleAspGlySerAlaPro 286  
Db 887 GGTCACTGTGGCGAAGTGTAAGCAAAGCAAGA-----GCACCTTCTGTGATGATCAAGAA 940  
Qy 287 ThrGluPheCysArgAlaValAspAlaAatqProAlaMetGlyValSerAsnAsnTyrrPro 306  
Db 941 ACCAAATTGTACATTTGCACTGATGGNAAGTCAAGGTTGCACCTCTACCCCA---CCC 997  
Qy 307 GlyLeuLeuGlnAsnMetThrTyrrHisAsnSerThrIle-----GlyGluIleAla 323  
Db 998 GGTTACTTTGGCAATGTGATATTACAAACACACCTATAGCTGTGGCAGGTGATCTGATG 1057  
Qy 324 AsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGluLeuAspProAlaSerMet 343  
Db 1058 TCAAAACCAACATGGTATGCTGCAAGCAGAATCCACAATGCATTG-----TTA 1105  
Qy 344 ArgGlnArgThr-----ArgGlyLeuAlaThrTyrrLeuHisAsnAsnProAspLys 360  
Db 1106 CGAATGGACCAACGATATTATTTGNAGATCGGCTCTTGACTATCTAGAACTGCAACCCGATCTA 1165  
Qy 361 SerAsnValSerLeuThrAlaAspAlaAaspProSerThrSerValMetLeuSerSerTyr 380  
Db 1166 AAGCGCTGTTTGGGGGCTCATCTTTCAAGTGTCAAACCTTGATATCATGACTAGTGG 1225  
Qy 381 AlalysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuGlyLysProGluThrVal 400  
Db 1226 ACTAGGCTTCCAATCCATGATGTGACTTGGTGGGA-----1264  
Qy 401 ArgArgProIlePheGlu-----ProValGluSerLeuMetTyrPheMet 415  
Db 1265 ---AGGCCAATATTCATGGGACCTGGTGGAAATTCATACAGAGGGGCTATCTTTCAATAAT 1321  
Qy 416 ProLysLysPro--AspGlyGluPheCysAlaAlaLeuSerLeuArgAspGluAspMet 434  
Db 1322 CCAAGCTCAACCAATGATGGAGCCTATCTGTGGCCATAGCTCTTCAGCTGACCATATG 1381  
Qy 435 AspArgLeuLys 438  
Db 1382 AAGCTGTTTTAAG 1393

RESULT 15  
US-10-425-114-298  
; Sequence 298, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 298  
; LENGTH: 1753  
; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700071662\_FLI

US-10-425-114-298

## Alignment Scores:

Pred. No.:	7,08e-10	Length:	1753
Score:	173.50	Matches:	98
Percent Similarity:	33.62%	Conservative:	59
Best Local Similarity:	20.99%	Mismatches:	157
Query Match:	7.43%	Indels:	153
DB:	16	Gaps:	19

US-10-614-954-6 (1-451) x US-10-425-114-298 (1-1753)

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QY 69 AsnThrGlyThrSerPheIleValProPheGluAspValProArgValValVallysAsp 88
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Db 176 AACTCCAACTCGACCTCGTGGTGGCGGCTTCCACACGCCCGAGTGTCTACTTC-----229
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QY 89 LeuArgAspAspProSerAlaProThrIleGluGly-----MetArg 102
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   |||
Db 230 TACCGCGGACGCGCCCGTGGCGGCGGAGGGTTCTTCGACGGCGAGCGTATCGCG 289
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QY 103 LysAla-----GlyTyrProMetAla-----109
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Db 290 CGCGCGCTGCGACGAGCGCTCGTGGCTTATCCAAATGGCGGGCGCTCGCGCGGAC 349
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QY 109 -----109
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Db 350 GAGGACGGTAGGTCGAGATCGACTGCAATGGCGAGGGAGTGCTTCTTCGAGGCCGAC 409
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QY 110 -----MetPheAspGluAsnIleAlaPro-----ArgLys 120
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Db 410 GCGCCGATGCTCTGCGATGACTAGGTGACTTCGCGCCACCATGAGCTCAAGCGC 469
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QY 121 ThrLeuProIleGlyProGlyProAspAspProLysProValIleLeuLeuGln 140
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Db 470 CTCATCCGACCGCTCGATTACACCGACATCTCGCGCTTCGCGTACTCGTGTCCAG 529
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QY 141 LeuAsnPhelIleLys---GlyGlyLeuIleLeuThrValAsnGlyGlnHisGlyAlaMet 159
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Db 530 GTGACTATTATTCAAATGTGGAGCGCTCCCTGGTGGTGGCATGGCAACCATGACGG 589
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QY 160 AspMetValGlyGlnAspAlaValIleArgLeuLeuSerLysAlaCysArgAsnAspPro 179
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Db 590 GATGGCATGCTGGCTGCACTTCACTAATCATGTCTGACCTTCGCGTGA-----643
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QY 180 PheThrGluGluMetThrAlaMetAsnLeuAspArgLysThrIleValProTyrLeu 199
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Db 643 -----643
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QY 200 GluAsnTyrThrIleGlyProGluValAspHisGlnIleValLysAlaAspValAlaGly 219
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Db 644 GCTCAAAATTTCTGTCATGCGCTTCATTTGACCGGACCGCTTCTTCGTGCT-----691
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QY 220 GlyAspAlaValLeuThrProValSerAlaSerTyrAlaPhePheThrPheSerProLys 239
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Db 692 -----CGTGATCCCAACCACTTCATCTTTCAACATATCGAGTACCGCT---736
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QY 240 AlaMetSerGluLeuLysAspAlaAlaThrLysThrLeuAspAlaSerThrLysPheVal 259
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Db 737 -----GCCCGAGCTATGTTGCTCCCAACCCAGTTCCTT 772
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QY 259 -----259
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Db 773 GCTTCCAAGTCAAGCCACCTGCCATGCTGTGGACATTTTCAAGCTCACTCGCTCAGAC 832
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   |||
QY 260 -----SerThrAsp 262
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   |||
Db 833 CTGGCGCGGCTGCGCTCACAGCTTCCTGACGGGAGGTGACCCCGGTTTCAGCACATAT 892
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QY 263 AspAlaLeuSerAlaPheIleThrLysSerAlaSerArgValArgLeuGluArgIleAsp 282
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Search completed: January 24, 2005, 10:54:26

Job time : 814 secs

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Db 893 GCAGTGCTAGCGGCACATGTCGTGAAATGTGTCTCCCTTGCAAGC-----AGCTACTCT 946
QY 283 GlySerAlaProThrGluPheCysArgAlaValAspAlaArgProAlaMet-----Gly 300
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Db 947 CCTGNAACACCCACCAAGTTGTTGCGCCACTGACGCCCGACACGCGTACAGCTCCA 1006
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QY 301 ValSerAsnAsnTyrProGlyLeuLeuGlnAsnMetThrTyrHisAsnSerThrIle---319
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Db 1007 CTACCAAGATGGGTACTTTGGC-----AATGTCACTCTTACCGCGACACCACTTGT 1057
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QY 320 -----GlyGluIleAlaAsnGluSerLeuGlyAlaThrAlaSerArgLeuArgSerGlu 337
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Db 1058 GAGCGCGGCAAGGTGACCAAGTGA---CTGGCAGAGGAGGAGCAGTATCCAGGAGCA 1114
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QY 338 LeuAspProAlaSerMetArgGlnArgThrArgGlyLeuAlaThrTyrLeuHisAsnAsn 357
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Db 1115 CTGGATAGATGGAC---AACGACTACTGCGCTCAGCGTTAGACTACTCTGGAGCTTCAA 1171
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QY 358 ProAspLysSerAsnValSerLeuThrAlaAspAlaAspProSerThrSerValMetLeu 377
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Db 1172 CCGGATCTGTCAACACTTGTGCGTGGAGCGCATACCTTCCGCTGCCCGAACCTAGGCTC 1231
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QY 378 SerSerTyrAlaLysValGlyLeuTrpAspTyrAspPheGlyLeuGlyLeuLysPro 397
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Db 1232 ACCAGCTGGTGGCGCTTCCTATCCATGCTGACTTCGGATGGGC-----1279
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QY 398 GluThrValArgArgProIlePheGlu-----ProValGluSerLeuMet 412
   |||
   |||
   |||
Db 1280 -----CGGCTGTGTTTCATGGGGCCAGGTGGATTGCGTATGAAGTCTGGCG 1327
   |||
   |||
   |||
QY 413 TyrPheMetProLys---LysProAspGlyGluPheCysAlaAlaLeuSerLeuArgAsp 431
   |||
   |||
   |||
Db 1328 TTTGTCTCTCCCAAGTGCAAAATGGCGACGCGACGCTGTCCATTTGCTATCTCTGTGCAAGCT 1387
   |||
   |||
   |||
QY 432 GluAspMetAspArgLeuLys 438
   |||
   |||
   |||
Db 1388 GAGCACATGGAGAAGTTCCGG 1408
   |||
   |||
   |||
```